

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number.

TO: Barba Kroma

Location: REM-2B692C18

Art Unit: 1638

Friday, September 03, 2004

Case Serial Number: 10/732721

From: Deirdre Arnold

**Location: Biotech-Chem Library** 

**REM 1A64** 

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

#### **Search Notes**

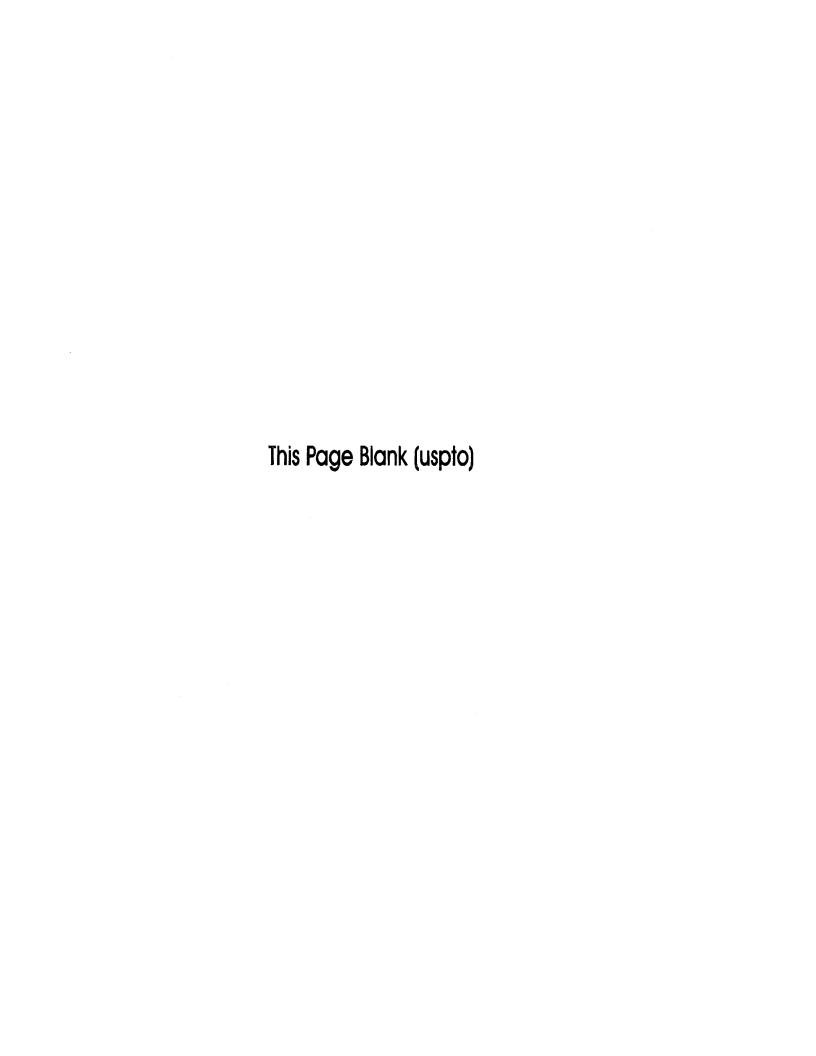
Thank you for using STIC's	ervices.		
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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions repm and runpn Searches run against the Amino Acid Pending database produce two sets of results, with the extensions searches run against the Amino Acid Pending database produce two sets of results, with the extensions searches run against the Amino Acid Pending database produce two sets of results, with the extensions searches run against the Amino Acid Pending database produce two sets of results, with the extensions rapm and rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.



OM nucleic - nucleic search, using sw model

September 2, 2004, 06:48:28; Search time 6301 Seconds (without alignments) 11404.975 Million cell updates/sec Run on:

US-10-732-721-1 1658

Title: Perfect score:

1 gaattcacggctcacaatac......tcgttagtttgggacggcg 1658 IDENTITY NUC Gapopt 1.0 Scoring table: Sequence:

3470272 segs, 21671516995 residues Searched: 6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

GenEmbl:\* Database :

9b ba: \*
9b\_htg: \*
9b\_ov: \*
9b\_ov: \*
9b\_pr: \*
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9b\_pr: \*

90 sy: \*
90 un: \*
90 un: \*
91 un: \*
92 un: \*
93 un: \*
94 un: \*
95 un: \*
96 un: \*

sts:\* em un:\*

em vi: \*
em htg hum: \*
em htg inv: \*
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em htg vrt: \*
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em\_htgo\_mus:\* em\_htgo\_other:\* em\_htgo\_hum:\*

~ed. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequen	34041 Danio	90608 Huma	1569 Zea	Zea mays	uat		AFISI389 Dermacobi	Dermaconi	== .		AL929356 Flasmodiu					ALS90608 Human DNA		AC115612 Dictyoste	25	ത്	AR116777 Sequence	AE001381 Plasmodiu	Continuation (5 of	ion		Homo	Ratt	nna	AE014820 Plasmodiu	AE014839 Plasmodiu	AX345159 Sequence	ACL41/18 Apris mein	ACUUSSUS Flasmodiu	AEU1485U Flasmodiu	AC144975 Silurana	BX537131 Danio rer	AL035475 Plasmodiu	Ξ.	nuation	12 Di	1355	n,	5093 Danio	7 Zebrafi
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ALIGNMENTS

PAT 22-MAR-2003

linear

AX655393 2000 bp DNA Sequence 5263 from Patent W003000898. AX655393 1 GI:29158207 Oryza sativa RESULT 1
AX655393
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.

REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                      697 ITTGTTTTCTCTGTGCTTGCGATGATG--CAGTAAAATAAACGTGTGTATCTCATGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     755 TGATCGACGTGTGTCGGCGATTTCAAATCAGTAACAATCACATGTGCATCCCCATCGACT
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                                                                                                                                                       Gaps
                                                                                                                                                      3,
                                                                                                                              Length 2000;
Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)
                                                                                                                                                    Indels
                                                                                                                         ch 4.1%; Score 68.8; DB 6; ... [ Similarity 11.8%; Pred. No. 9e-05; 81; Conservative 310; Mismatches 292;
                                                             /organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1054 CTGATTCTTTGTTACTATATGGTGCT 1079
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HTG; HTGS PHASE1; HTGS DRAFT.
Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                      Local Similarity
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Direct Submission Submitted (10-NOV-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 149818; sum-of-contigs
Insert size: 169833; 6.1% error; agarose-fp
Quality coverage: 4.15x in Q20 bases; sum-of-contigs Quality
coverage: 3.89x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
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75196 75195: gap of 100 bp
90316 90415: gap of 100 bp
90416 95884: contig of 5469 bp in length
95885 123970: contig of 5469 bp in length
95885 123970: contig of 27986 bp in length
23971 124070: gap of 100 bp
24071 12749: contig of 27386 bp in length
27450 127549: gap of 100 bp
17550 150918: contig of 23369 bp in length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2196: contig of 2196 bp in length 2296: gap of 100 bp 26907: contig of 24511 bp in length 66907: gap of 100 bp 6528: contig of 9421 bp in length 66328: gap of 100 bp
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of 18035 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 145795 bases at least Q40
Consensus quality: 147142 bases at least Q20
Consensus quality: 147142 bases at least Q20
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2297. .26807
/note="assembly_fragment:00741
fragment_chain:I"
26908. .36328
/note="assembly_fragment:00183
                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                     Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="DKEYP-95D10"
/clone lib="DanioKeypilot"
1. .2196
                               Actinopterygii; Neopterygii; Tele
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 150918)
                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
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26807:
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Fri

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TERBEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPORTANT: This sequence is not the entire insert of clone RP11-363F12 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-363F12 is at 1 in this sequence. The true left end of clone RP1-244F1 is at 198338 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr6
RP11-363F12 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chcri.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="TIGGER1 repeat: matches 2151. .2279 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4615. .4996
/note="LiMA9 repeat: matches 5378. .5759 of consensus"
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/note="L1PA7 repeat: matches 4697. .6123 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="17 copies 2 mer aa 82% conserved"
9287. .9336
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10742. .10832
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13160. .19307
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/note="MER77 repeat: matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens'/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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/clone lib="RPCI-11.2"
723. .955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL590608 200337 bp DNA linear PRI 21-JUN-2001
Human DNA sequence from clone RPI1-363F12 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200337)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 CACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATT
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Pred. No. 0.0025;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes"assembly fragment:00076
fragment chain:3"
5988. 123370
/notes"assembly fragment:00925
fragment chain:4"
124071. 127449
/notes"assembly_fragment:00103
fragment chain:4"
127550. 150918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00560"
                                                                                                                                                                                                       /note="assembly fragment:00131
fragment_chain:2"
72512. 75095
/note="assembly fragment:00059
fragment_chain:2"
                                36429. .54463
/note="assembly_fragment:00422
fragment_chain:1"
                                                                                                      54564. .65123
/note="assembly_fragment:00239
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                  chain:1"
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          ragment
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Best Local Similarity
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/note="TIGGER1 repeat: matches 1. .1967 of consensus"

//note="FLAM C repeat: matches 1. .133 of 23533. .25472

23400. .23532

repeat\_region

repeat\_region

Direct Submission Submitted (21-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 23, 2001 this sequence version replaced gi:14529950.

DEFINITION

AL590608

ACCESSION

VERSION KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

.144 of consensus"

/note="AluY repeat: matches 1. .311 of consensus"

26263. .26589

repeat\_region

Fri Sep

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.6131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                #4686. .44934

/note="LIP repeat: matches 4985. .5244 of consensus"

/4956. .45591

/note="LIPBA" repeat: matches 5527. .6162 of consensus"

/note="LIPBA" repeat: matches 4952. .6280 of consensus"

/note="LIMA" repeat: matches 4952. .6280 of consensus"

/note="MEM6A repeat: matches 1. .140 of consensus"

51192. .51609

/note="LIMBS repeat: matches 5721. .6166 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6152 of consensus"
                                                                                                                                                                                                                                                                                                                                                              .6313 of consensus"
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6091. .76275
                                                                                                                                                                                                                                                                                                     complement (40758. .41162)
/noce=match: STS: Em:HSPA31G7"
/noce="LiMC1 repeat: matches 5440. .6313 of consensus
44021. .4382
/noce="LiMC1 repeat: matches 4662. .4985 of consensus"
/noce="LiMC1 repeat: matches 1662. .4985 of consensus"
/noce="Alux repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote="Alusp repeat: matches 150. 194 of consensus" 5319. 53458
53019. 53458
58019. 58307
58019. 58307
58107
5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818. 5818.
                                                                                                                                     Thote="114 copies 2 mer ta 63% conserved"
30299. 30585
Anote="AluJb repeat: matches 3. .282 of consensus"
30272. 37393
Anote="114 anote | matches | 1388 | .6131 of consens 88096 | .38328
Anote="114 copeat: matches 60 | .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77189, ,77705
/note="MEK68A repeat: matches 6. .559 of consensus"
78243. ,78536
                                                                                                                                                                                                                                                                  1842. .51877

note="18 copies 2 mer ca 83% conserved"

3075. .53224

note="75 copies 2 mer ta 73% conserved"

3085. .53240
                                at 64% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6963. .77076
note="57 copies 2 mer tt 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="6 copies 26 mer 72% conserved" 3264. .53308
                                                                    80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 5962.
                                                                                                    note="21 copies 26 mer 61%
29354. .29515
/note="81 copies 2 mer a
29441. .29518
/note="3 copies 26 mer 8(
29738. .30283
                                                                                                                         0044. 30271
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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87399. .88707
/noce="LiPAl6 repeat: matches 5443. .6157 of consensus"
88710. .88750
/noce="LiR28 repeat: matches 13. .53 of consensus"
88727. .89132
/noce="MER61C repeat: matches 14. .431 of consensus"
                     /8889. .79139
/note="LiPB1 repeat: matches 5894. .6154 of consensus"
/9671. .80056
                                                                                                                                                                                                                                                      /note="THEIC repeat: matches 1. .371 of consensus"
80188. .80485
/note="LTR18B repeat: matches 220. .603 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                 7449. .87759 note="MER67C repeat: matches 106. .414 of consensus" .7781. .87889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER67C repeat: matches 410. .709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89148. .90930
/note="MEK61-internal repeat: matches 2814. .4549 of
                                                                                                                                                                                                      .292 of consensus"
                                                                                                                                   /note="Alusx repeat: matches 1. .262 of consensus" 82491. 82744 //note="MIR repeat: matches 2. .261 of consensus" 85379. 85469
note="AluY repeat: matches 1. .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.7%; Score 60.6; DB 9; Length 200337; llarity 50.9%; Pred. No. 0.022; Conservative 0; Mismatches 139; Indels 0;
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Best Local Similarity
Matches 144; Conserve
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/codon_start=1
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GRNLDQDFAEVVPQAPMGTRSQAGVPLAGVGCAALVDHLRAASWPSKFRPHLPEKYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSNPSEFLOVYVTALTAAGGNTAMMATYFHVALSGPARTWLMILSFGSIYSWEELYAR
YRDPSARVOOHGVBAHLIARVRQPEPRETLENFTSFTKVOGTIPREDSASIITARROS
VRDBKMLEKLATHVORILYPTLLALDKCARAABGRAWHLAPOTGATOSGGSGAIPRDBOK
KKEKKENKDRDHQKPRSTALVVAVGTGGRGDRNKRPRPQRGNSGSCPVHPWGRHNTVECR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (49176. .49850)
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NJ 08855-0759,
                                              1 (bases 1 to 78101)
Song, R., Llaca, V., Linton, E. and Messing, J.
Sequence, regulation, and evolution of the maize 22-kD alpha zein
gene family
  Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="similar to Zea mays cl locus myb homolog CDS and
                                                                                                                                                                                                                       2 (bases 1 to 78101)
Llaca, V. and Messing, J.
Direct Submission
Submitted (27-OCT-1997) Waksman Institute, Rutgers,
University of New Jersey, P.O. Box 759, Piscataway,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="cosmid contig; inbred line BSSS53"
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                                     clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="inbred line BSS53"
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/db_xref="taxon:4577"
/chromosome="4"
                                                                                                                                                           Genome Res. 11 (11), 1817-1825 (2001)
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/clone="III.4H10"
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10872. .73554
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/chromosome="4"
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'db_xref="taxon:4577"
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9689. .9
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                                                                                         AUTHORS
TITLE
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Library Committeed (04-SEP-1998) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
J (bases 1 to 65155)
Silaca V., Lou,A., Young,S. and Messing,J.
Direct Submission
Mission Nov-1998) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
A (bases 1 to 346296)
Song,R., Llaca,V. and Messing,J.
Direct Submission
Submitted (12-APR-2001) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
Sequence update by submitter
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
Song,R., Llaca,V. and Messing,J.
Direct Submission
Submitted (24-APR-2001) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
Mino acid sequence updated by submitter
On or Defore Apr 12, 2001 this sequence version replaced
gi:4416300, gi:44140643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60320 AATGGAGCATICGIGCIGATAACGIGITAAGAACCCITTGCIACIAGIGGIAGICGAAAGG 60379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60380 CTTCTTAATTAGAATAGAATCATAAACACAGGAGACACAAATGTATAGGAGGAACTGTT 60439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60440 ATTCTTATTCATGTATT-CAGCTCATTGGTTACAACAAATGGTGGTGTCCTCCTCTATAT 60498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="MATKILALLALLKLFVSATNAFTIPQCSLAPSAIIPQFLPPVTS
MGFEBHSAVQANKLQQALAASYLQQPTAQLQQSCLAHLTIQATTTQQQQQCFLPALSHLA
MVNPAAYLQQQLLASNPLAANVVANQQQQQLQQFLPALSQLAMVNPAAYQQQQLLS
SSPLAVQRAPFYLQQQQLLQQIYPALYQLAVANPVAYLQQLLEPNQTLSNSAAYLQQR
QQLLNPLVBANPLVBARFLQQQQLLFYNQFSLMNPVLARQQPIVGGAIF"
SSPLVVGNAPTYLQQQLLQQIVPALTQLAVANPAAXLQQLLPFNQLTVSNSAGYLQQR
QQLLNPLAVPNPLVTAFLQQQQLLPYSQFSLMNPALSWQQPIVGGAIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTAGAGCCACGTGCTGATAACGTGTTAAGAACCCCTTGTTACCGAGTGTAGTCCAAGG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1002 CTGCTTAACT--GAATAATAGTAGAACACAAGGAGACAAGAGTGTAGAGAGGAACTGATT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060 CTTTGTTACTATATGGTGCTGCTCTCCAAAGGTTACATGATATGGGGATCTCCTCTAT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1120 TTATAGACAAAACTAGGGTTTCAGGCATATGGGCCACATAGGCCTTCCTGGCCCAAGAAA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLN 14-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (Dases 1 to 3aes, Andropogoneae, Zea. Song, R., Llaca, V., Linton, E. and Messing, J. Sequence, regulation, and evolution of the maize 22-kD alpha zein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arusu447 Zea mays 22 kDa alpha zein gene cluster, complete sequence
                                                                                                                                   complement (67340. 68552)
/note="similar to Zea mays globulin-1 promoter" 68037. 68563
/note="similar to Zea mays globulin-1 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.6%; Score 59.8; DB 8; Length 78101; Similarity 62.3%; Pred. No. 0.027; 0; Conservative 0; Mismatches 92; Indels 5;
                                                                                                                                                                                                                          71597. 72372

/note="similar to Zea mays zrp2 promoter"

/gene="azs22-10"

/gene="azs22-10"

/gene="azs22-10"
                                                                                                                                                                                                                                                                                                                                                                                          product="22-kDa alpha zein 10"
protein_id="AAC01577.1"
db_xref="G1:2832247"
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21549079
                                                                                             note="22-kDa alpha zein 9"
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Song, R., Llaca, V. and Messing, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60557 GGTTTCTTAACACTCCC 60573
                                                                   'gene="azs22-9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1180 GGTTTCTTAACACTACC 1196
                                                                                                                                                                                                                                                                                                                                                                          codon start=1
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                                             38815. .59610
                                                                                                                   psendo,
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Best Local Simi
Matches 160;
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VERSION
KEYWORDS
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206778 ATTCTTATTCATGTATT-CAGCTCATTGGTTACAACAAATGGTGGTGTCCTCCTCTATAT 206836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206658 AATGGAGCATTCGTGGTGATAACGTGTTAAGAACCCTTTGCTACTAGTGTAGTCCAAAGG 206717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1059
IFGALALASQLWPRHFPLTDGALCLVAATAFTAELVLFYFHSTTHMGLEGYYHYLLVL
                     LVGLCVAAAVLGALLPDSFPADLASGVLVALQGLWFYQTALALYGPMLPAGCARDADA
HVECRSRAAQGRAEQLAISQLFALVLLAFLYALGCYAVAAARYGRPPELPAVRHRRAA
AVELECRQGDDAGAMEECAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1120 TTATAGACAAAACTAGGGTTTCAGGCATATGGGCCACATAGGCCTTCCTGGCCCAAGAAA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 AGTAGAGCCACGTGCGTGATAACGTGTTAAGAACCCCTTGTTACCGAGTGTAGTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTTAACT - GAATAATAGTAGAACACAAGGAGACAAAGAGAGAGAGGAGGAACTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206718 CITCITAATTAGAATAGAATCATAAACACAGGAGACACAAATGTATAGGAGGAACTGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1060 CTTTGTTACTATATGGTGCTGCTCTCCAAAGGTTACATGATATGGGGATCTCCTCTCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="nested in grande 1 retroelement"
/rpt family="copia-type retroelement PREM-2"
/rpt type-dispersed
complement(50572. 50576)
/note="target sequence duplication"
complement(50577. 52000)
/note="copia-type retroelement PREM-2"
complement(552949. .>56140)
/product="copia-type pol polyprotein"
complement(52949. .56140)
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                                                                                                      /rpt_type=dispersed
complement(39147. .39151)
/note="target sequence duplication"
/note="target sequence duplication"
/rpt_family="gypsy/7y3-type retrotransposon"
/rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="copia-type pol polyprotein"
/protein_id="AAD20307.1"
                                                                                                                                                                                                                                                                                                                                                                     complement (45973. .49223)
complement (49224. .49228)
/note="target sequence duplication"
complement (50243. .550571)
/note="similar to grande 1"
complement (50572. .60252)
                                                                                                                                                                                                                                                  complement (39152. .42406)
complement (42452. .45283)
/note="gypsy-type polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.039
0; Mismatches
                                                                                         complement (38797. .38910)
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                                                                                                                                                                                                                                                                                                                         /pseudo
/codon_start=1
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300001
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Best Local Similarity 62.3
Matches 160; Conservative
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PFMAL6F1 00
PFMAL6F1 01
PFMAL6F1 02
PFMAL6F1 03
PFMAL6F1 04
PFMAL6F1 04
PFMAL6F1 06
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PFMAL6P1 13
WPCOMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                              join(<11112. .11154,11262. .11396,12254. .12344,14272. .14410, 14838. .14890,18185. .18230,18599. .>18657)
/product="hypothetical protein"
join(11112. .11154,11262. .11396,12254. .12344,14272. .14410, 14838. .14890,18185. .18657)
                                                                                                                                                                                                                             CGSGCGGGCGGGGGGGGTGTMANBGQSRSGGVGTLLSSNAMGGBGQQAHSAGCGSGCGGGC
GSGMVIBGSKANNAMSGGCGSGCGGGCGSGMLIEVSKANNAMSGGCGSGCGGGGGGG
VNBGSKANNAMSGGCGSGCGGGCGALFNASTAAGBGLHNKSAGCGGGGGGGGGG
                                                                                                                                                                                                                                                                                                 CGSGMAIEGFKANHAKSGGCGSGCGGCGTLFSSSAAAQQGSRSGGCGSGCGGGGGS
SRNYAEGSNAGGACGGGGGGGGGAGTTLEALMGADYVAEQESGTA
RCEELVGPATTPPTATIFYGCKKSLQRFACGACDGGDGELSFPLAKPVEINBVLHN
YVIAPDSRLHAKDIVNPQHDFVVETCCCCSSTSPWLAAAASSLQNAFEGTKEQTAATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVEGVQHDMAPQREVLLGRDMIGRSTSRTCSVGTWSVAPPRGLARYITEPLLEMLSF
DHRPCPYAGLGGVEIFEKRKTVLDPSLFHYYQESAVTNLYEALDNRDGILSRQLLRSI
GMEDPKVKTVLKNQEAISLMKSIKDPQAAAK"
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EAMIKGLRPGPSAQYFARKPPQTLEKLLQKMDEYIRADNDFRQRREEAFRFSEMTRGF
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FGDQPRRIFCLFCGENKGHTTRMCHVTIQKQKEIAEAAAAQAQPQGIMHTASYHSPYI
PEYVGNHPAVSVASASQPQASWHQPPPPPPLQQGQQPEGGQYAQHQRDFREQSEARTV
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PAPGPARLLELYVVAGGALADMCVEVLYSTHLRIFAGGEVNPAHLNDLEHGGMLLMFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MSYQATVSSYGGNTAVMAKSFVMVVRSVAQTWYSSLRPGTITSW
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oin(3179. .4286,5020. .5155,5266. .5443,5892. .6020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to cell division protein FTSZ"
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31759. .31763
/note="sequence target duplication"
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oin(36233. .36579,37382. .37925)
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db_xref="GI:4416307"
                                                                                       /evidence=not_experimental
/product="hypothetical protein"
/protein id="AAD20310.1"
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.2614)	.2656)	.2690)	.2807)	.2856)	.2929)	n" (2987)	.3070)	.3142)	.3454)	.3376)	.3504)	.3597)	.3692)	)n" .3928)	(0868.	.4056)	.4288)	
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163990 Tartaattigcaaraacgcgaaaaraccaaaaaaaaaaaaaaaaaarttcaaacaattraaa 163931
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AF151389.1 GI:7159047
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Lessinger.A.C. and Azeredo-Espin,A.M.L.
Direct Submission

Direct Submission
Submitted (14-MAY-1999) Centro de Biologia Molecular e Engenharia
Genetica - CBMEG, Universidade Estadual de Campinas - UNICAMP, Lab.
Genetica Animal, CBMEG, UNICAMP, P. O. Box 6109, Campinas, Sao
Paulo 13083-970, Brazil
1. 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 CAATATACAAATTTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATC 184
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Bukaryota, Metaroa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Oestroidea, Oestridae, Dermatobia.
                                                                                                                                                                                                                                                                                                                            Query Match 3.4%; Score 56.4; DB 3; Length 273275; Best Local Similarity 51.6%; Pred. No. 0.22; Matches 129; Conservative 0; Mismatches 121; Indels 0;
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Evolution and structural organisation of
Evolution of mylasis-causing flies
Med. Vet. Entomol. 14 (1), 71-80 (2000)
20221065
                                                                                                                                                                                                              /locus tag="PF14 0709"
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4395, 4436
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Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases I to 328)

Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.

The mosaic structure of variation in the laboratory mouse genome
Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                              12 TCACAATACCAGTCATCTACATGTGATAAATTTTTATAGTTAGATTACTTCTTGTAATCAT
                                                                                                                                                                                                                                                                                             72 ITCAGAGGATGAAAAAAAATCGCAAGAAAGCAAATAITITAAATGATGATGCAATATA
                                                                                                                                                                                                                                                                                                                                                                               132 CAAATTTAAATTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCT
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S212P6542FG4.T0 CZECHII/Ei Mus musculus STS genomic, sequence
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0
                                                                                                                       3.4%; Score 56; DB 3; Length 1792;
49.3%; Pred. No. 0.073;
tive 0; Mismatches 150; Indels
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                 43. .1612
1613. .>1792
/product="12S ribosomal RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerstin Lindblad-Toh
'product="tRNA-Ile"
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Mus musculus
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Fax: 6172580903
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Submitted (14-MAY-1999) Centro de Biologia Molecular e Engenharia
Genetica - CBMEG, Universidade Estadual de Campinas - UNICAMP, Lab.
Genetica Animal, CBMEG, UNICAMP, P. O. Box 6109, Campinas, Sao
Paulo 13083-970, Brazil
Location/Qualifiers
                                                                                                                                                                                                                                                                                                0;
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Lessinger,A.C. and Azeredo-Espin,A.W.
Lessinger,A.C. and Azeredo-Espin,A.W.
reylution and structural organisation of mitochondrial DNA control
region of myiasis-causing flies
Med. Vet. Entomol. 14 (1), 71-80 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CAATACCAGTCATCTACATGTGATAAATTTTATAGATTAGATTACTTCTTGTAATCATTTC 74
                                                                                                                                                                                                                                                                                                Gaps
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Oestridae; Dermatobia.
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/organelle="mitochondrion"
/mol_type="genomic DNA"
/strain="Alfenas"
organism="Dermatobia hominis"
                                                                                                   complement(<1. .42)
/product="LRNA-11e"
43. .1612
.1612. .1791
/product="12$ ribosomal RNA"</pre>
                 organelle="mitochondrion"
/mol_type="genomic DNA"
/strain="Ponta Grossa"
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complement(<1. .42)
                                                                               /db_xref="taxon:115427"
complement(<1. .42)
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                                                                                                                                                                                                                                                      3.4%;
Similarity 49.5%;
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AF151388/c
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Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                        97 AGAAAGCAAATTITTAAATGAATGATGCAATATACAAATTTAATTACAAATTTATGTAA 156
                                                                                                                                                                                                                                                                                                                                                    ATAATACAAATATATAATATATAATATAAAATATTAAGTTTAATATATAAATATAA 153
                                                                                                                                                                                                                                                                                                                                                                                             GATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATTAA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                152 GGTATAAATGTAAAGTTTAATATAAATAGGTTGAGGAAAACTGATTAGTCAATTAAGGCA 93
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Mashington University Genome Sequencing Center Center code: WUGSC
Web Site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                .
0
                                                                                                                                                           Length 328;
                                                                                                                                                   Score 55.8; DB 11; Length : Pred. No. 0.052; Dr Mismatches 97; Indels
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Trani,L., Cotton,M. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-342E23
/mol_type="genomic DNA"
/srain="C2BCH11/Ei"
/db_xref="taxon:10090"
/map="+ 19 33-281 29021847-29022095"
/clone lb="C2ECH11/Ei"
<1. .>328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGCATATGTATTAAGCGAAAAAAAAAAA 62
                                                                                                                                                                                              0; Mismatches
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Sulston, J.E. and Waterston, R.
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3 (bases 1 to 125316)
Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                       3.4%;
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AC092635
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Mapping information for this clone was provided by Dr. John D. McBherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-132H1; the clone sequenced to the right is RP11-375H3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-342E23; actual end is at base position 65825 of RP11-375H3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of AC041020 has been incorporated into AC092635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Data from AC073062 was used to finish this clone, AC041020.
                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise
                         Center project name: H_NH0342E23
Summary Statistics
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/clone_lib="RPCI-11"
43. . 13.7
/rpt_family="AcHobo"
397. .636
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/db_xref="taxon:9606"
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1476. .1623
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1. .125316
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2964. .3035
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                                                        Drafting Center: WIBR
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'rpt_family="L1"
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Plasmodium falciparum 3D7

Plasmodium falciparum 3D7

Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,

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Cronin,A., Davis,P., Dear,P., Clark,L., Clark,R., Corton,C.,

Cronin,A., Davis,P., Dear,P., Dear,P., Doggett,J.,

Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N.,

Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,

Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larke,N.,

Lawson,D., Lennard,N., Line,A., Maddison,M., Mclean,J., Mooney,P.,

Moule,S., Murphy, L., Oliver, K., Ormond,D., Price,C., Ouail,M.A.,

Rabbinowitsch,E., Rajandream,M.A., Ruther,S., Rutherford,M.M.,

Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R.,

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Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                              94026 ATGTACTGAGTTTTGTATTACACATACAGCATTAAATTGTATTAGAAATAGCTTACAGGA 94085
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AL929356 AL844508
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Submitted (20-SEP-2002) P. falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 158, UK
For more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AUGIGALAAATITIALAGITAGAITACTICIIGIAAICAITICAGAGGAIGAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                    92 TCGCAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTACACAATTA
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Nature 419 (6906), 527-531 (2002)
22255708
                                                                                                                                                                                                                                                  Length 125316;
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/ Caring lation = "WRI SHEEF IGRKQYKSCRKSKKKKI FSPPDCFVNTNFKI PKKK
WIJKEI KKONFORGETVUSRCYSNI DGNI EENI EI EERKGNEKQSND ILFDEMHRKKKG
KONFILLSKONSTYGSEVUSRCYSNI DGNI EENI EI EERKGNEKQSND ILFDEMHRKKKG
KONFILHTSNYKOPERTLKONI PROKEVUS HOOT II YNVILKND I INDITILETFPEDDA
LSNVILHTSNYKOPERTLKONI PYNKLARVHIKNKLI INLYTSKINNI YSNLI-FYHTYKNK
NIHVVANI I IHMEKKY INLYTNANNAN INRET YLYTYKERKKKRAFHIK INDIK
NIHVARNI I HMEKKEKK I HNYLFKINNAN FORT INNST TANDROM STANDIN SIIN
RINNYSELKSINI INNYDMPHHEINREKKRYKYELLE HYYYKEI BYNNON FILIDRENV
KNOF FPFFYHTLI CGEPT FPF INREKKRYKYELLE HYYYKEI BYNNDIF II DRENV
KNOF FPFFYHTLI CGEPT FPF INREKKRYKYELLE HYYYKEI BYNNDIF II DRENV
TNYPRNI SFF FGKRKNNKI INLITRNRK PY PINLINNNELKYNST INKELSYILYNK
TNYPRNI SFF FGKRKNNKI INLITRNRK PY PINLINNNELKYNST INTENTIN TNYPRITTENT
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2 probable transmembrane helices predicted for PFI0340c by
IMHMM2.0 at aa 511-530 and 542-561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISFNKINFLTDLFILKNVEHINLSYNTFMNVESNMTSHGITKDINNMDEKNDIYHNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Hypothetical protein. Pfam match to PF00560,
see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                      complement (join (496. .1978, 2292. .4594))
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                                                                                                                                                                                                                                                       _xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leucine Rich Repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="possible exon'
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             /gene="PF10330c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /qene="PFI0330c"
                                                                                                                                                                                                                                                                                               chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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Ф.
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                                                                                      Source
                                                                                                                                                                                                                                                                                                                                          gene
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                                       FEATURES
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SKSLCKLMREFYSMLIENGNIYNNTNNNNNNNNYYYYYNNNKKNDDILFFRGIYF
SEWIILFLNKIFNSLISEEEKIPIENWTFIIDLMKMYYUDKNIILQYVQKKNDYVFFP
                                                                           YDMENTHYKIKKYNYEEKNMNVDHNMCNIYONOSISRYEEKKNEEDISYFECANTLLF
TNILKDYYKNPHKVTKTYFSFPHVFFNCIIKGLKDEDVKRKLYVVNHIIPKELNEDGF
YKNIITTCVFIFFHIKQFNDIIEYEKVIYLLKKIINLNLTDTFSSVLFYFILNADMDK
                                                                                                                                                                                                 EKTTDEYHNVINNCNITEDENKKMSPSKKSTYTSNHYTKGEFIEVSNKQINYLLKTNY
IIENIFYYLHLYNGEKECKILLTSLLNYIRPFIKLIEDNKNENLNNMSNKLLYICIYN
                                                                                                                                                                                                                                                                                 NKIYVLLNILLINIVELHNWNYFFIERFFNPTSKYCFGLCYGICILDIINHIIYRNSLT
VFSLFKNFQMKKKKILMYISRMKVEEVGRGGEKKKKKKKKKKKSYLELINELDEKSNMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIERNNIIEDNNHDILRLNEKNENYEEANFRLCQTIIVLPKLIKECDILCYISVDMYK
VLFSINNITCNNKNEEYIMTYKLFAIVLLCIHSPIEICKYMFNNIYNNIYDNIQKALM
ILCFQLTALYLSSRIKLDEIYDYIKNINKTMNISERLIRGNKAMDSKTNDKIDLLDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFIDLCNIYFSGVYSTLFSFKIKKEMSKIDYDEYRIFKYYSEDFTLTTYLLSSYNTFL
NCCNNYYLYLEDIIQDGFSLVHVFINSDKFMIRRACCKLLYDMINLIFCKKMFYILKN
QNYEIYEYYENVMNYISNRIKQERDSLSYEYMKQILSIYRTIKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NININDNINKAVANNINDINKKIDDI DYNINDNI DYNINDNCYSYDKYNILHUDCNNQHSGN
NPDNDNINININMMASVDLENETKFLEDWEVTQKKI YDPT I GLRKHYTNELLSCGEKINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RILEKWSSMVNRDI VWFHKAHFTTLERRVKGI POKTEWKI WFHITHNAKULINGKOKK
YYLSKKKSWYTULLIDISRTFPELLI FDKYAOOLYFVLARYSWYSEPSYGYCOCMY
FLVGLLI I SHPNEHETFTCHLYDISRTFPELLI FDKYAOOLYFKERFPLARF I YLFERIMONEI P
LVDHFNNEEVYPPVTHQWLLTLFIADFIKSVI VIMDYLFSTSIKKI III SYALLKI
LKSTAKKHFREKILLKLIKSLKXNBSNDDILI ARLITIKSSI SILLSNELLYLFRRIEND
HVPFNSQYKF I IDNI TTCHFRHI QENI TOMNITHNCINNYDTENDTTHNQDNNNNNNNG
HVPFNSQYKF I IDNI TTCHFRHI QENI TOMNITHNCINNYDTENDTHNQDNNNNNNNGN
NNSNNNNNNNSYNYKKKYRYSHLI NEDSNFVILDGVPLINFFSHNI LKKKNBEBLKFT
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AYHDVLSSLKESNSVHNISDEENPNHPNLKDHNNKYYKNNIATDNSNDHMDMYWMKEN
NQEENINNMNSINNMNSINNMNSTNSINNINNINSIDYINYNNYNNYNNSLNSSHASV
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GDNNVNSYKKENEQMKNI KYLNDSKEKENI FI HMNNKEGHNDEQKENI KHKHREDENE
DEEKEEEEEEE I LNI SQYI SYNEKETSSKONNNDNEKNDDNNNFGFFSLINSYAKDNS
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KLDAYEKKYKIISDDIDKLTKEIQLALELEQTSNINKNNINQDDDDHNSKNVFVRPDG
FLEIREEYHSSDEENNKHNVKNEKINSLSSNINEIQEKIIKREDDITNINRNENKKDD
ERTQHDEKHKIIKNKSININKQGILNIQENYTSSSSEIDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WENMCKEINHFDEEKNIQIQEDEVEEEIDNVDVEKRIHVCSIKKFNKSCCLVNKKKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MSELKPLELEYLDKNVKKKKKEKDEKKKNLNKIFMNRKHSFKKE
GSDNTDVHEQNILENDKNEKNEKNDNDIMNSNKENDNKDGKSIFHSFSINKIFGEKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKSLNQKPQNDHENINKTHTKHIANDKENVGEYHMINQNIKNHHMHELNMCDNDHKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MMDEKAYIKDYEIEKATQRLFLKLKNEKIKEDILRKSINEYKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="TBC / Rab-GAP domain. Pfam match to PF00566, TBC domain; SMART hit to SM00164, Domain in Tre-2, BUB2p, and Cdc16p. Probable Rab-GAPs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFDVSTINKYYQFNKKDVDRELDNINSTEKKEYNDTDLVDDAHTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /produčt="hypothetical protein"
/protein id="6A551755.1"
/db_xref="G1.23504972"
/db_xref="SPTRRMBL:Q1379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon start=1
/product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="SPTREMBL:Q81378"
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/db_xref="G1:23504973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="GOA:Q8I378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="PFI0345w"
15885. .19286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="PFI0345w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="PFI0350c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="PFI0350c"
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gene

CDS

complement (21948. .24716)

gene

gene

CDS

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126

246

306

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79906 TATAGAAAATAAAATAGAAGTAAAACAAGTACAGTTTCAGTATTGAAAAAGGAACACTA 79965
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Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (Bases I to 25313)

2 (Bases I to 251313)

Gardner, M.J. Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T., James, K., Elsen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Manguoli, S., Petrea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M., Fairlamb, A.H., Frantlamb, A.H., Frantlamb, A.H., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE014846 253132 bp DNA linear INV 11-FEB-2003 Plasmodium falciparum 3D7 chromosome 12, section 3 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ACGGCTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79666 ACTGTAAATGAAATCAATAATTATTTAATTATACCTATTGCTATATTATTATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATACAAATTTAATTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 ITTCTAGAGTCATAATAATGCCTAAATTAAAATTCTATTCTATTTTTCCTTAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Hyman,R.W., Fung,E., Conway,A., Kurdi,O., Mao,J., Miranda,M.,
Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                         DB 2; Length 205429;
                                                                                                                                                                                                                                                                                                                                                                                           155; Indels
192427: gap of unknown length
203864: contig of 11437 bp in length
204064: gap of unknown length
205429: contig of 1365 bp in length.
                                                                                                                                 1. .205429
/organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                  0.43;
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.43
0; Mismatches
                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                            Score 55;
                                                                                                   Location/Qualifiers
1. .205429
                                                                                                                                                                                                                                               /clone="PFYAC357"
/clone="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum 3D7
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                                                                                                                                                                                                                                                                                                                                              Query Match 3.3%;
Best Local Similarity 48.8%;
Matches 148; Conservative
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AE014846 AE014188
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       192228
192428
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AE014846/c
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AUTHORS
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JOURNAL
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KEYWORDS
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                                                 /Gene="PPI03550"
/gene="PPI03550"
/gene="PPI03550"
/note="C-terminal half of protein is similar to prokaryotic ATP-dependent heat shock proteins. Similar to Rhizobium loti heat shock protein, ATP-dependent his protease ATP-binding subunit, helu ml15004 SWALL:Q98CU1 (RMBL:AP003005) (443 aa) fasta scores E(): 8.5e-54, 46.69% id in 439 aa, and to Escherichia coli, and ATP-dependent hel protease ATP-binding subunit helu or http: or b3931 or 55478 or ecs4058 SWALL:KSLU ECCLI (SWALL:B32168) (443 aa) fasta scores: E(): 2.1e-51, 46.56% id in 451 aa. No HWMPfam hit; SMART hit to SW00382, ATPases associated with a variety of cellular activities"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205429 bp DNA linear HTG 12-AUG-2000
Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
PROGRESS ***, 4 unordered pieces.
AC005506
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.

Direct Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="ATP-dependent heat shock protein, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 ACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAAAAAA
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HTG: HTGS PHASE1.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases I to 206429)
Hyman, R. W., Fung, E. L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Aug 12, 2000 this sequence version replaced gi:8810449.
* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 335050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55.8; DB 3; Length 3
Pred. No. 0.32;
0; Mismatches 102; Indels
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Plasmodium falciparum 3D7 chromosome 12
                                  .24716)
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                                     complement (21948.
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                                                                Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M.,
Nakao, B., Rowley, D., Tamaki, T., Mang, F. and Davis, R.W.
Direct Submission
Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
Location Qualifiers
outwhitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA 3. (bases 1 to 253132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MSRRVNYYEVLGVPQDADLTVIKKSYRTLAMKWHPDKNPNNKAE
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DGGSCFTSVETSTSANGGKFKNRVVKTSTSKSTSIINGKRVTRIETVKTLPNGTVERTV
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/db_xref="G1:0n="WIVLIRKNNLKNTLRIPPLGCNNKLVFWRGYINEQTKGPIEKKT
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NREELKITRNIFERINKKKKHVSNLSYKDIYIDPYWNPFKDVDNLKQEILYEFNEYSK
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RRMALYPYDKKPEKDDLIPLMDPLQFLLDSLIHRYIQLNDLRAQAIIKVMINRYPSLN
YYKYFFYSSKKEKDKNEKTAQNEQEENVSEKKEPFSQMLQKYKKNYYENFYKY"
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DISLSIKKKKKKKCTKONLLLLANSINDI KSBDSL&PI PEPTNNI BEKQDENBINDILKL
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SDPLNQINSDLLNI DDPLLINNMYI I KKYKKGDTSNVDMSNVDMSNVDI SNVDPSNKD
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FTIEDFLVHNNFMNKYEIYRNIVINNFFPIQMNKNGDHKKKKINNNNNKKKYIDHE
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STFYAHWYNNENGKKIKSFKIYRVNLLCDKIRVRAARKMRNFLFIGDSCNDEYQKDIK
SEDQQKSNNNYVSDDTNEKDSDYFYNNDILKEDKQINNNILLDDTYHKEILFNNNHVK
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ENGKILYLKEKKGINKYNNEKDMMCNHSAFDNNMVQNNNVLDNMCNKKNIKKKMKKKKKKKKK
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ENKKQBKI I KKKELLI ILEKEI PKKLKEEKKLKEKEKKKEKEKFKFLKNBKEI KKK KED
KKRQKEEFLRKI KEEKKKLKEEKKKLKQE I INSI KEERKKFKELKSKFKKI SKKDNHL
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DIKNLKSLQKILRIKESKGKNKIETVVHIPNNVIERSVAKKIVLNKHEGIKNKDGVKE
KVKTKKKISLFGIVKPEDIIKRGINNVYHNIEDNQKLYTDVLIIGAGISGLAASYYLN
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KGKTKHEFANCTEFNNEKSMRKEDDIDYEDNFIWNMKKKKTKKKKYKVIVKKRYNYN
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KI KLRNNMLPMI KNNI DNI RNYFKI YNKEKKDNI LNFPKSLDED I HFYNNLSDSCYHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | VVDGWKWLINYLSEEVQNKIFLNTVAEL, VY IKDKHQDKKIYHLDNDNCQINKQKSSS
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KYVIVALPLGCLIENDKKRKLKTCLKFEPELHPLKLRALQNYKMGNHNKIILRFYPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(8355. 17090,17320. 17469)
/locus tag="PFL0575w"
/note="HMMPfam hit to PF01593, Flavin containing amine
oxidase, score 1e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="hypothetical protein"
'protein id="AAN36203,1"
locus_tag="PFL0570c"
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7668...7702
/rpt_type=tandem
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7629. .7664
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/rpt_type=tandem
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<8355...>17469
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TITLE JOURNAL

MEDLINE PUBMED REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

COMMENT

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74695 TATAGAAAATAAAATAGAAGTAAAACAAGTACAGTTTCAGTATTGAAAAAGGAACACTA 74636
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Plasmodium falciparum strain 3D7, chromosome 5, segment 2/4.
AL929352 AL844504
AL929352.1 GI:23504570
                                                                                                                                                                                NTDIINEDDKEISYPHEKMEEVNNMNOKKLSIALIKSNNVGNNNDDDNNNNNGHIQKS
NISTDELDIKKINLASKTKONNITNKKOVMIQTNLAIYNNIDLQNKIKOIYIINHEKIC
VLINDYLKVVLIHLESISKNILDEQIMSSNNNKMNSCGFIPFLCYILQYILKHLKYDLFN
STYNTKVVIQLLCDYIYYLIFCKHDILCYKCNNGGELANCDSYNCNNSWHTYCLISSEE
HNMNNKANDKFWLCPSCSNIDISKHVQRGCYNQNEIMENYWKRIYIYKIKPFLSRTRK
                                                               KQDKNINHIKNETDALKCSSYKKEIKSNTYESFTNNSLINFEDKKSNDVKSNISTLLL
NLYEYNNKSTDQIHYFDRIKSIDSYKSKYKNGSYLLELHSKDSENDSNKNDANNICTI
                                                                                                                ETFNNVDKONKGDHINDVHNDVYNDVYNDKYTSNYNIETYSHITNNHFEYINNISNLY
INKYMIKLNDAVFYNYNEIENTILNKQHNAEYNKSYFVLLQTFSNIFKKYSDFTYFIQ
KELFLKIQAMKHILFNDNNFQSLQDMNVVLSQAEHKNDHIVSHNNHMNDVDRKKAYEQ
RVVFCGEYLSKSYFOCVDGAYDTGIRAAEDIAHIGLHLKNNDTKNYKTDVYIFPQNKC
                      PFTNIPLPPIKKKFLGFYITDGSDEALTDYESSSDENMNTNVDINIDINSNTNIDINN
                                                 NTNSNTSSNINNNTNKYNYCNNNI PI SVMKKEY EFLLYSLQSIQNI FRFLKKQNTHKN F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ACGGCTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 3;
Pred. No. 0.45;
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/rpt type=tandem
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                                                                                                                                                                                                                                                                                                           IRKRLDLLKAHLSRSVA"
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8510..8652
/rpt_type=tandem
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/rpt_type=tandem
8428. .8498
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Best Local Similarity
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PFA929352/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ð qq ò g à d à g ð Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C. Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N.,

Plasmodium falciparum 3D7 Plasmodium falciparum 3D7 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

ORGANISM

REFERENCE AUTHORS

ACCESSION

KEYWORDS VERSION

gene

CDS

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HYTKEWRGKMYTKDIVTHFYNLDTMTYMNKINKHIDNVTLNNDDNYYTYDNINGSHG
NIPERKHLYLKSKVKIDGSDHFSVPTLAGSKRYTGFYNKOBELGNGFRFGVP
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NYNNTIKLGSTNYTLOSDDWINGYNDKOBLONGFLGNEBLGNGFRFGVP
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SEKOGLGVDYDYTGCTILDKKINIINKYTYKCSLGANSHSLEPINYNBLYYGGSNNGNAEL
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SNNMSCEVISLYNBITNVKYMNGKYEHVFFLTYDNKLFGIGNNKNCQLLCDNEKENNY
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HNNINBQHIRTKRININI INSNYI NHTYNYEQUNALKKYNSKDI QNKKYSFYKNSSNYLCS
FI EDLYADFRNBRVRI FI FILKLIE BIKNSLNYHSI FNIDTSI FFTLI OMLEFKK
BILINFAQCLI DLDNPRNSFYTLLIOQLSKKVPKNI DLNQQSVSNAKNNOHTKHLQTNI
PMYGSAHRRENLLI NDMYNDRMVVDKNI HVKNSTHMDLKNDGANKKKKIKKKKNNKKK
Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S.,
Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D.,
Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N.,
Lawson, D., Lennard, N., Line, A., Maddison, M., Molean, J., Mooney, P.,
Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A.,
Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M.,
Sanders, M., Stamonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R.,
Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and
Barrell, B.
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IKHPFKIIKWLYYDQKDLDYNGSGSDBEJNEYNTYNNWYSNYNYIKINETEITUVRKNI
NTTELFQNEYTYFGYTEEEIENFINJIVNNIINWCHLQNLIKKEEYNNNMEYIKES
EKDIIDLYSKHIEVLLINLNIYEKQFNYLYTNYQNFIISNIANMKEQHLDNILYPFSTY
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SGDDIYSGDDIYSGDDIYSGDDIYSGDGINHSVNKLNKKKNVKREPNISSFIDNLNDD
EKDKEFLNFIKGKTQNESDKKRLFVNDISCYKSGVPYNIPNINMEDENMYRNNISQEI
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KEKEKKKKKKKKKNDI KKEEKEENNINNEKKNNNNNNIN INSEKKKKNDINGHEAKYVQNK
KFFYNEHNFKNDIGLPSDDDIYDDYNISGDESLLNFEADNISSIQNEDTNMDEDVYNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Similar to Plasmodium falciparum guanidine
nucleotide exchange factor pfrccl (1327 aa) fasta scores:
E(): 9.6e-190, 97.459% id in 1338 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="guanidine nucleotide exchange factor, putative"
(protein id="CAD51450.1"
(db_xref="GI:23504571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-5EP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Thinxton, Cambridge CB10 189, UK
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pain, A.,
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devlin, K., Baker, S., Davies, P., Mungal, K., Berriman, M., Hall, N., Bowman, S., Churcher, C., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Plasmodium falciparum 3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="genomic DNA"
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/gene="PFE0420c"
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gene

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QEI CEBUKKEI QKVKENMSNYKVI TERNNLESRLERLKILFARKI KITTUPITUREKHITEN LAITEN LAITE
                                                                                                                                    FHYHLINRNSYYYOLKILPQVCHIFNLFRFQNYLMLSFNDPALDIVNFFYTYKNNIPIO
KHKHKHTLNSTMVGTNKMDIQKERERHLNIKCLGKDMCNIQRPKGVSTFGTHQDNKKI
NSNECNESLLRKAKNDNLNDRFEMKEGKGMINGVMKRGDNPMGGYNIMGGNNPMGGYN
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| db_xref="SPTEMBL:Q31416"
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| Ab_xref="SPTEMBL:Q31416"
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| AT TAINS LOT="MYNIFNY YENDERENKYKKKKEDSKKYSUDDSYNKTINNITYNDHKTDE
| SSYAYKKASSYHWHRENY PDERRKKYYEHIGKUNRESYDYSSNYDESDFSSTSSY
| YNERNKKYYKKEDKKKKEKEKEKEKEKEKRKYYHHTDDDQDHLESYSSSRSSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFKDDKILQKSKARQIYFDMLQNTYDKSSFPQVKWRNIALQISLNILRKKKHMNYLKK
LYBKQBYIEDLIINYQHKMKKDIVTLKNAIIFVSKLYIEKPILLHSSYFKKNLFPVBL
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CDFLBILYLNKYESLNIYNLNIISIKYIFEHTFISLTNVINNICNTHHHIYVDAYTNL
                                                                                                                                                                                                                                                                                                                                                                                             PMGGNNPMGGYNPMGGNNTMGGNNPMGGYNPMGGYNPMGGYNPMGGYNPMGGNTNEAN
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TNNLI LKLKSLKMNYMSLQDQKENNLIHLI NKA I DI FLSDEMTYVEFLDEFPANLSI Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFNLPSTIKITSNDNKMRKKMKRLIFSEDDIEFFIKCKLIYNVKLDIRFLLKEKNMSI
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YHNYESDEETINKDESNNININININININININKDSSSENLINKTHEQREKSININKI SKEN
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DVKESNIYPYTIHNSNNNMFEDKNSGISKNMSKKNNTNEKKNTNQYTDITKVEQEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKONDTMELSLKAKKINELMKTYNFLSLOBNHDKFLKNAQYEBFDKIABKEALKVTEH
IKDEKEKKLIFNKTKEDIKKKLIQNKIQSDTMNESIQRNMLLSALRTKOMKKYSPYLP
HTYITEDNNILLEBFYINNYPQHVRLKISHKDVLAKIADMSGATCQIKGQYSNPSQPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Weakly similar to Arabidopsis thaliana FBn16.20
protein fBn16.20 TR:Q9ZV23 (EMBL:ACO05727) (332 aa) fasta
scores: E(): 2e-12, 28.763% id in 299 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONFLLDTKQLHIBILAPTYNQIQIARNELNSLLNNFMISCNIKAKRASTGWAPP"
complement (16588. .17442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Similar to Rattus norvegicus RNA helicase TR (EMBL:U25746) (1032 aa) fasta scores: E(): 2.4e-59, 38.387% id in 719 aa" codon start=1 /product="ATP-dependent RNA helicase, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="hypothetical protein"
/protein_id="CAD51451.1"
/db_xref="G1:23504572"
/db_xref="SPTREMBL:Q81417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9222. .10010
/gene="PFE0425w"
9222. .10010
/gene="PFE0425w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLHNFVIDLY
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199536 AAAAATTAAATGTTTATATCAATTTGTAACATATAAATGTGAACATACAAAAAAATGTAT 199477
                                                   /note="Similar to Rickettsia prowazekii single-strand
binding protein ssb or rp836 Sw.SSB RICPR ((92CC2) (152
aa) fasta scores: E(1: 1.1e-16, 38.158% id in 152 aa
Signal peptide predicted by SignalP 2.0 HMM (Signal
peptide probabilty 0.896, signal anchor probability 0.017)
with cleavage site probability 0.471 between residues 25
and 26"
                                                                                                                                                                                                                                        /codon_start=1
/product="single-strand binding protein, putative"
/protein_id="CAD51453.1"
/db_xref="SI:2504574"
/db_xref="SPTREMBL:QB1415"
/translation="MGKRMLCIVFPLLIYFNYVLHRTYGYIIGDVKVHQLNNIINKRI
                                                                                                                                                                                                                                                                                                                                                                                                             IKSRKISMFKINLQNDFNYENKRFYNNMNRNVMNEKSLNKIMLIGRVGCEPDIKILNG
                                                                                                                                                                                                                                                                                                                                                                                                                                   GDKVATFSLATNEFWRDRNTNELKSKTDWHRLVVYDQNIVDLIDKYLRKGRRVYVGGS
LHTRKWHTNDMNSQPKQITEIILSYNKGDLIFLDDKRNFNQRNNSNNINSENQOHINN
EHINNNNINNGNDFWPLNSNDKIIEDKEFTDRLDDNNEENNFQSNSETFDKQEGIYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein id="CAD5144.1"
/b_xref="fg1:2350454.1"
/db_xref="sPTEMBL:08141"
/trānslation="MSTCNNIVDLVRNKKELLTGEKKMRKKSCNIDRNTIDNENNKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKNILINNFINSEKLIKEIQLINNISLRSATYLLKIEIEKIQKLISCNNWKQVPSIYK
KSAENILLKKNEYIKNLKTKLINKNKAIQNNINNDNIDNIDNIYNSCYNLVNKNDEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSKHLNSSSSSSSLSSYSSLSNPSDDSCFSNKQNQNNFFSNIKCNNSYFTGNAQTKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDNHTSKKKTKINDKIYDKIYDKINDKICDKKYDKIYDKKYDKKYDKKYDKICDKICDKKYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIYDKKYDKKYDKIYDKICDKKNDIKNDKNIKTFNVKGKDTKIIKLDKEHVKDKINYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PFE0440w"
/note="Weak similarity to Plasmodium falciparum Pfc0425W
protein pfc0425W TR:077336 (EMBL:298547) (4550 aa) fasta
scores: E(): 7.2e-23, 22.792% id in 3238 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                  gene="PFE0435c"
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/gene="PFE0440w"
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Search completed: September 2, 2004, 09:38:04 Job time: 6308 secs

'gene="PFE0435c"

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2, 2004, 06:07:12 ; Search time 639 Seconds	(without alignments)	11022.711 Million cell updates/sec
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US-10-732-721-1 score: Sequence: Perfect

1 gaattcacggctcacaatac......tccgttagtttgggacggcg 1658

3373863 segs, 2124099041 Searched:

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

6747726 of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003bs:\* N\_Geneseq\_29Jan04:\* geneseqn2003as:\* geneseqn2003cs:\* geneseqn2004s:\* genesegn1980s:\* genesegn1990s:\* geneseqn2000s:\* geneseqn2002s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rice gene Human imm Signal tr Chemicall NBP46 (ro Human imm Human imm Human imm Human met Human gen NBP46 (ro Haematopo Chemicall Human imm DNA trans Tumour su Human bre Human che Human met Description Ada71938 Ab132257 Ab132257 Ab132257 Aas61275 Aax08223 Ab134174 Aas46772 Abc07549 Ab134206 Ab134206 Ab134207 Abc134207 Abc134207 Abc134207 Abc134207 Abc134207 Abc134207 Abc134207 Abc134207 Abc134307 Abc134307 Abc134307 Abc134307 Abc134307 Abc134307 Abc134307 Abc134307 Abc134307 Abc134308 Abc134208 Abc134308 Abc134208 Abc134308 Abc134308 Abc134308 Abc1493308 Abc1493308 Abc134308 Abc1493308 Abc1493300 Abc134308 Abc1493300 Abc134308 Abc1493300 Abc149330 Abc1493300 Abc14933 AAX08523 ABL32303 ABL34174 AAS46772 ABT07549 ABL33206 ABL34552 ABZ10246 AAS45498 ABL34107 ABK28430 ABN80224 ABL70328 AAS61275 ABL34584 DB Query Match Length 6265 12763 113515 17280 1134 15767 15767 17142 17142 17142 8067 14551 6012 6012 49.4 49.2 49.2 2222211111111111 222221111111111111 Result No.

2001324K	Aban6279 Sov bean								_	_	~	144	Human								DNA tr
AAS61087	ABA06279	ABA06275	AAN60472	ABL32763	ABL34163	ABL32902	ABL33275	AAQ27886	AAS45371	ABK28208	AAS45477	ABL34022	ABQ67006	ABQ66972	ABL32694	ABL32570	ABK33948	ADA20352	ADA84159	ABL34175	ABK28227
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48.6	48.4	48.4	48.4	48.2	48.2	48.2	48.2	48	48	48	48	48	48	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.4
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## ALIGNMENTS

ADA71938 standard; DNA; 2000 BP. (first entry) 20-NOV-2003 ADA71938; RESULT 1 ADA71938 

Rice gene, SEQ ID 5263

Plant; bacterial infection; fungal infection; viral infection; rice; ds. dene;

Oryza sativa.

03-JAN-2003

WO2003000898-A1.

22-JUN-2001; 2001WO-IB001105.

22-JUN-2001; 2001WO-IB001105.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Ġ Hou Y; SA, Hou Zhu T, Goff Glazebrook J, Goff Whitham S, Xie Z, Cooper B, S, Tao Y, Chen W, Co F, Quan S, Chang H, Ch Katagiri F,

WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression

Claim 27; SEQ ID NO 5263; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to

Haematopo Human lym Rice gene DNA trans Human pol

ADA71938 ABK28428 ABL49380

48.8

ABZ10042 ADE84086

1501 1501 2000 8961 8961 gene;

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neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                      WO200200928-A2
                                   Homo sapiens
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                                                                           03-JAN-2002.
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                                                                                                                                                                                                                                   CWYRGKGYYWAGMWMKRYKRMYMYKMMWYKRKYSKCSWYCKMSYYASCMKSARKAGAKM 601
                                                                                                                                                                                                                                                         CTGCGCGCGTGCTAGCACGCGACGTCGACGCTGATGCTAGCGTTGCTACTTTTGTT 696
                                                                                                                                                                                                                                                                      842 RGRARKARYWWKWATWCATKRWMTKGKGAKWAWTWMAKAWRKYYWSWMRAWYYYYKTRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   755 TGAICGACGIGIGICGCGAITICAAAICAGIAACAAICACAIGIGCAICCCCAICGACI
                                                                                                                                                                                                                                                                                                                                                        GMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWKMWRRYATRMMWWYRYSMKWYT
                                                                                                                                                                                                                                                                                                                                                                                    WCIMWGYWWYWWRIYMKOMRYMWYKCIKTYWWWSAIYWIGIWAAWWMAKIKMRMGMIGAKI
                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAGAATAATATTACATAAAATA-TGAGTTCAACATCTTTCTTAATACCTTTTGCTCG
                                                                                                                                                                                         MCTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKAR
                                                                                                                                                                                                                                                                                                  TITGITITICICIGIGCTIGCGAIGAIG--CAGTAAAATAAACGIGIGIATCICAIGIGAI
                                                                                                    GGCGCTTTGTATTCCTCAGCAGCTCTGCGCGCCCCGTGCTTCGTGTACGGCAGTGACGAGG
                                                                                                                                                                         CAGCAGCAGCTCTACGTGCCCACGTGCCTGCCTGCCCACCGTGATGGCAAGGCTTG
                                                                                                                                                                                                                CTTGCTTGCGTGCGTGTGGCAGCGACGAGGTTGAAGCTACGGCGGTGGCTGCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; anticilammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                    'n
                         Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                               DB 7; Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system associated gene SEQ ID NO: 230.
                                                 ie-06;
292;
                                                                   Conservative 310; Mismatches
                                              4.1%; Score 68.8;
11.8%; Pred. No. 1e
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ABL32257 standard; DNA; 7498
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                                                           Local Similarity
      illustrate the
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                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid theukaemia, Alzheimer's disease, ANDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 230; 32pp + Sequence Listing; German
                                                                                                                                                                           Berlin K;
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02-JUL-2001; 2001WO-EP007537.
                                               30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                     Nucleic acid comprising diagnosis and treatment
                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                           Piepenbrock
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RESULT

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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligomucleotides and/or DNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be contained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in parafich such as tissue from eyes, intestine, kidney, chan, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal changing the complex of the invention are useful for the diagnosis and cancer. ABN311545 represent
  transduction associated disease; solid tumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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Pred. No. 0.023;
0; Mismatches 128; Indels
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CpG island; signal transduction as:
antitumour; cytostatic; mutant; ds.
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                                                                                                                                                                                                           29-JUN-2001; 2001WO-EP007472
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 50.2
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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                                                                             3 ATTCACGGCTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCT
                                                                                                                               123 IGCAATATACAAATTTAATTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAA
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                            DB 6; Length 6012;
Sequence 6012 BP; 2120 A; 32 C; 1149 G; 2711 T; 0 U; 0 Other;
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is convicted the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The commission of the provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences grown in records ABL70111-ABL70626 represent chemically pre-treated sequence data for this patent is not represented in the printed sequence data for this based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1179 CCTACAATAAAATTACAATAACCAACTCCATAAAATTTTCTATTTACGATAAAAAT 1120
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                                                                                                                                                    cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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                                                                                                                    Chemically treated cell signalling DNA sequence complementary to#109.
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Pred. No. 0.023;
0; Mismatches 128; Indels
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                 ABL70328 standard; DNA; 6012
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01-SEP-2000; 2000DE-01043826.
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                                                                                    01-JUL-2002
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                                                  ABL70328;
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and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences from chemically modified genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene requiation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours
                                                                                                                                                                                                                                                                                                                                                                                     Gene regulation-associated gene; severe combined immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                  cardiac damage; inflammatory response; Haemophilia; Merner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Precelampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; coseophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
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                                                                                                                                                                                                                                                                                                                                           Human gene regulation-associated gene oligonucleotide #230.
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                                                                                                            1059 ATATTTCACCGTCTTAA 1043
                                                                  243 AAAAACAGCCCATTAA 259
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07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; transferion; fertilizer; ss.
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                                                      Gaps
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Length 6012;
Score 52.2; DB 6; Length 6 Pred. No. 0.023; 0; Mismatches 128; Indels
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    3.1%;
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4294. .4385
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1560. .1616
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1791. .3034
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1023. .1151
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    Query Match 3.1
Best Local Similarity 50.2
Matches 129; Conservative
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
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                                                                                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 AAAAAAAAATCGCAAGAAAGCAAATATTTTAAATGAAGATGCAATATACAAATTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12763 BP; 3481 A; 219 C; 3026 G; 6037 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1%; Score 50.8; DB 6; Length 12763; 56.6%; Pred. No. 0.072; ive 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AATGCCTAAATTAAAATTCTATTCTATTTTCCTTAAGAAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 276; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 276.
                                                             3485 AAAATAAAAATAATTATTCAACTTTT 3457
                                 292
                                264 CCATTAGAATGCGCGCTGCTCCATTTTTT
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                                                                                                                                   ABL32303 standard; DNA; 12763
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2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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94; Conserv
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                                                                                                                                                                                                                                                    immune
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01-SEP-2000;
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                                                                                                                                                              ABL32303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to modulate oligoarcharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
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Pred. No. 0.037;
0; Mismatches 136;
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Best Local Simi
Matches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis, and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11402 AAAATAAACAAATTAATAATATATTTTTCTATTTTTTTAAATATTTTTACAATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified gene, useful f
with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 CATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAA
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                                                                                                                                                                                                                  system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113515;
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               The present sequence is a gene of the invention
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                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 2147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of chemically of diseases associated
 Score 50.8;
Pred. No. 0.
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                                                                                          DNA; 113515
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51.8%;
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01-SEP-2000; 2000DE-01043826.
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diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130909/17.
                                                                                          ABL34174 standard;
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                                                                                                                                                                                                                     immune
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Best Local
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                                                                               ABL34174/
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acidioner (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or prognesis events which are disadvantageous to for diagnosis and/or prognesis events which are disadvantageous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragments of chemically modified genes associated with tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene derived chemically modified sequence #496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17280 BP; 4730 A; 151 C; 3624 G; 8775 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour suppressor gene; oncogene; antitumour; cytostati
tumour; CpG dinuclectide; single-nuclectide polymorphism; SNP;
cytosine methylation; ds.
                                                                         11282 TACAATAAATATATAAAATTTCTTTTAAATCAAATTCAAAA 11241
205 IGCCIAAAITAAAATICTATICTATITITCCTIAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                         AAS46772 standard; DNA; 17280 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-WAR-2000; 2000DE-01013847.
06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                           AAS46772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             olek A,
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DB 4; Length 17280;

Score 50.6;

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TATITICAGAICIGAAGITAAATITIAAATITIGAIGAGITIAAAGITIAAITATITITI 15047
                89 TCCAAGAAATTCTATTATAAATAAGTGTACTTTTACCAATTCCATTGTATAAGCAAACAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disporters, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, atteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 CGCAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTAT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarteritic; antidabetic; antipsoriatic; antiarteritic; antidabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                             131 ACAAATTTAATTACACAATTATGTAAGATTACATTGTTTAGTTTTCATAGAAATCAATTTC
                                                                                                        TGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15767 BP; 4558 A; 123 C; 3384 G; 7702 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                                                                                                                                                191 TAGAGICATAATACCTAAATTAAAATTCTATTCTATTTTTCCTTA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.0%; Score 50.4; DB 6; Length 15767; 19.3%; Pred. No. 0.099;
                                                                                                                                                                                               209 CAGACTACTAAATTTGGCATAAGAATAATTCTTTTAAAATGCAACATA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1179; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 1179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                            ABL33206 standard; DNA; 15767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP007537.
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132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation.
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                                                                                                                                                                                                                                                                                                                                                          ABL33206;
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Best Local S
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                                                                                                                                                                                                                                                                                     ABL33206
ABL33206
XX
AC ABL3
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                                                                                                                                                            98 GAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTATGTAAG 157
                                                                                                                                                                                                                                                    158 ATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATTAAA 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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                                                                       CTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGAAGTTCTAGTCAATTTAATTTGATCCAATAAGTTTTTCTGAATCTCCTTTTTAAGT
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; breast specific protein; breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer associated coding sequence SEQ 1D NO: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1134 BP; 418 A; 141 C; 170 G; 405 T; 0 U; 0 Other;
       Pred. No. 0.091;
; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.032,
); Mismatches 111, Indels
                                                                                                                                                                                                                                                                                                                                                                                        5244 CAACTAATACACTAAAAATTAAAAAAAAAAAAAAACC 5208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X,
                                                                                                                                                                                                                                                                                                                                              218 ATTCTATTCTATTTTCCTTAAGAAAAAAAGGCCC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50.4; DB 6
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gene therapy; cytostatic, gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 171; 367pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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  52.1%;
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                          113; Conservative
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Best Local Similarity
Matches 113: Conserv
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Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Matches
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15168 TTGAAATTAAATTTTTTATTTAAATTAAATTAAATTGTAAAATTAAGTGTATTTAGAG 15227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enables a
                                                                 TIAAAAITCTATTCTATTTTTCCTTAAGAAAAAAAACAGCCCATTAAGGGACCATTAGAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining the cytosine methylation state and/or single incleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements, and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pelet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cpf distinguishes between methylated and non-methylated cpf represent specifically claimed nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between halthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between actue.
GTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAA
                                 15108 GTAATGTTTGATTGTTTTATTTTGGTGATGTTTATTTAAGGTCGATTTGTTTTAAA
                                                                                                                                                                                                                                                                                                                                                      Haematopoietic cell proliferation disorder related DNA seguence #386.
                                                                                                                                                                                                                                                                                                                                                                                         Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphocytic leukaemia and acute myelogenous leukaemia; as probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, 1
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P, Grabs (
Model F, 1
                                                                                                                                                                      15228 AAGITTIATATTTÄTTTTTTTTTTTTÄ 15255
                                                                                                                                      300
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                                                                                                                                    273 IGCGCGCTGCTCCATTTTTTTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C, Adorjan I
Lipscher E, Maier S, I
I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Distler J,
                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                         ABZ10246 standard; DNA; 8056
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                             16-JAN-2003
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Lewin A, Li
Schwope I,
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                                                                                                                                                                                                                                                                                             ABZ10246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention provides a number of human metastasis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCAAGAAAGCAAATATTTAAATGAATGATGCAATATACAAATTTAATTACACAATTAT
                                                                                                                          TTAAAATTCTATTCTATTTTTCCTTAAGAAAAAAAAACAGCCCATTAAGGGACCATTAGAA
                                                                                        GTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid derived from chemically treated metastasis genes, for diagnosis of cancers by analysis of cytosine methylation, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15767 BP; 4558 A; 123 C; 3384 G; 7702 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human metastasis associated gene SEQ ID NO: 105.
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                                                                                                                                                                                                                           15228 AAGTTTTATATTTATTTTTTTTTTTTA 15255
                                                                                                                                                                                             273 TGCGCGCTGCTCCATTTTTTATATA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one of the genes of the invention
                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                  ABL34552 standard; DNA; 15767
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2000DE-01032529.
2000DE-01043826.
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gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metastasis associated cytosine methylation;
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07-APR-2000; 2
30-JUN-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Best Local
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                                                                                                                                                             15168
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1527 TAAAAATITITAAATAAATITATITITITAAAAATITATAAAATITAAAATITIAAAATITAA 1586
                                                                                                                                                                                                                                                                                                                                                                                                                  1587 ATTTATATTATAATTTTAAAATTTAAAAATTGAAATAAATTGAATTGTAAAATTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell cycle; human, CpG dinuclectide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATT 214
                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                             95 CAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTATGT
                                                                                                                                                                                                                                      35 TGATAAATTITATAGTTAGATTACTTCTTGTAATCATTCAGAGGATGAAAAAAATCG
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disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemically pretreated genomic DNA associated with cell cycle #102.
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0
                                                                                                                      Score 50.2; DB 7; Length 8056;
Pred. No. 0.083;
0; Mismatches 93; Indels 0
                                                           Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 203; 28pp; English.
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                                                                                                                         3.0%;
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2000DE-01019173.
2000DE-01032529.
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                                                                                                                                                                              Matches 106; Conservative
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                                                                                                                                                  Similarity
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                                                                                                                         Query Match
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                                                                                                                                                     Local
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Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing

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                                                                                                                                                                                                                                                                                                              associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, leavy body disease, arthritis, arthritis, arteriosclerosis, solid tumours and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; noctropic; antianaemic; cytostatic; noctropic; antiarteritic; antiarteritic; antidiabetic; antipsoriatic; antiarterit; antidiabetic; antipsoriatic; antianatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                               17 ATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                               137 ITAATTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17142 BP; 5054 A; 299 C; 3741 G; 8048 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                 3.0%; Score 50.2; DB 4; Length 17142; 50.6%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                  0; Mismatches 118;
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01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                              Query Match 3.0
Best Local Similarity 50.6
Matches 121; Conservative
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                                                              of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAG 76
                                                           The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's pooriasis and inflammatory/ulocrative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                      3.0%; Score 50.2; DB 6; Length 17142; 50.6%; Pred. No. 0.11; tive 0; Mismatches 118; Indels 0;
                 Claim 1; SEQ ID NO 2080; 32pp + Sequence Listing; German.
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Best Local Similarity 50.6
Matches 121; Conservative
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137 TIBATITACACABITATGIBAGATTACATTGITITAGITTCATAGABATCAATTTCTAGAGI

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Sequence 33, Appl
Sequence 37, Appl
Sequence 777, Appl
Sequence 55, Appl
Sequence 651, Appl
Sequence 75, Appl
Sequence 74, Appl
Sequence 37, Appl
Sequence 3111, Appl
Sequence 3402, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
                                                                                2, 2004, 07:31:08; Search time 144 Seconds (without alignments) 6389.643 Million cell updates/sec
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Sequence 6, Ap
Sequence 56, A
                                                                                                                                                                    1 gaattcacggctcacaatac......tcgttagtttgggacggcg 1658
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-129-112-3

US-09-129-112-3

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US-09-641-638-651

US-09-641-638-651

US-09-642-290-1

US-10-204-708-75

US-09-16-204-708-74

US-10-204-708-74

US-10-204-708-74

US-09-916-421B-1

US-10-204-708-87

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US-10-204-708-6
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US-08-617-860B-32
US-08-617-860B-32
US-08-6323-170B-1
US-08-954-441-1
US-08-947-823-1
US-10-204-708-22
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Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1658
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Match Length DB
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48.8
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Sequence 3. Appli	ı	Segmence 63. April	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		Semience I Appl	Segmence 13. Appl	Seguence 1992. An		ì -	7	Segmence 538 Ann	Segmence 22. April	Segmence 1. Appli	Segmence 31. Appl	Semience 1 Appli	Semience 1 Apply	Sequence 1. Appli
US-09-801-861-3	US-08-319-704-5	US-10-204-708-63	US-08-973-462-1	US-09-790-988-1	US-08-916-421B-1	US-08-487-826B-13	US-09-134-001C-1992	US-10-204-708-10	US-08-545-528D-1	US-09-601-198-21	US-09-328-352-538	US-08-617-860B-22	US-08-107-755A-1	US-10-204-708-31	US-07-991-867B-1	US-08-544-332-1	US-09-370-861A-1
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41.8	41.6	41.6	41.4	41.4	41.4	41	40.8	40.8	40.8	40.6	40.4	40.4	40.4	40.4	40.4	40.4	40.4
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144 CACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATA 203
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Best Local Similarity 51.45
Matches 113; Conservative
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US-09-134-001C-777
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US-10-204-708-80/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Etzler, Marilynn E.
APPLICANT: Etzler, Marilynn E.
APPLICANT: Hurphy, Judith B.
APPLICANT: Hurphy, Judith B.
APPLICANT: Hurphy, Judith B.
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
TILE REFERENCE: 023070-079810US
FILE REFERENCE: 023070-079810US
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 TCATCTACATGTGATAAATTTTATAGTTAGATTACTTGTAATCATTTCAGAGGATGA
                                                                                                                     157 GATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATAGTGTTAAATTAA
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49.4%; Pred. No. 0.0012;
ive 0; Mismatches 136;
                                             Score 53.6; DB 3; 1
Pred. No. 0.0002;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                  1598 AATACTTTTTTAGTTTTTTTTTTTAATAAA 1567
                                                                                                                                                                                                                                                                                                                                   217 AATTCTATTCTATTTTCCTTAAGAAAAA 248
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Patent No. 6465716
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Best Local Similarity 49.4%;
Matches 133; Conservative
                                                 Query Match
Best Local Similarity 53.3%;
Matches 113; Conservative
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NAME/KEY: intron
LOCATION: (1152)..(1559)
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LOCATION: (1617)..(1697)
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2637..2750
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NAME/KEY: exon
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US-09-129-112-3/c
; LOCATION:
US-08-617-860B-33
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US-09-129-112-3
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: PIRENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT APPLICATION NUMBER: DS/10/204,708

CURRENT APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

WHERE OF SEQ ID NOS: 98
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                                                                                                                     153 GIAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAA 212
                                                            5927 iaraarararraarraaccacgaacriccriacaarrarraraaarararaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 CGCAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 48.8; DB 4; Length 8961;
51.4%; Pred. No. 0.0076;
ive 0; Mismatches 107; Indels 0.
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                                                                                                                                                                                                                                                 3485 AAAATATAAAATAATTATTCAACTTTT 3457
                                                                                                                                                                                           264 CCATTAGAAIGCGCGCTGCTCCATTTTT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (5096)
; OTHER INFORMATION: n is a or g or c or t
US-10-204-708-80
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APPLICANT: BOUGUELELY, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENSET.051CP1
TITLE OF INVENTION: GENSET.051CP1
CURRENT APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR PLING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR SPELING DATE: 1999-03-23
PRIOR SPELING DATE: 1999-03-23
PRIOR SPELING DATE: 1999-03-22
PRIOR SPELING DATE: 1999-03-22
PRIOR SPELING DATE: 1999-03-22
PRIOR SPELING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                     1686 ААААААААААСТААААТААААТТАААТСААСААААТАТТТТААААСААААТТАААА 7627
                                                                                                                                           143 ACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAAT 202
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                         203 AAIGCCIAAAAITAAAATICIAITCIATITITCCITAAGAAAAAAAA 250
                                                                                         Indels
                                    Score 46.4; DB 4; Pred. No. 0.035; 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: 1123_.3123
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 651, Application US/09641638
Patent No. 6432648
                                    Query Match 2.8%;
Best Local Similarity 54.8%;
Matches 92; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 5996..6099
OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 3124..3297
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 3871..4072
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 5552. 5633
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon 6
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OTHER INFORMATION: exon 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 7379..7522
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
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SEQ ID NO 651
LENGTH: 20674
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Sequence 777, Application US/09134001C

Patent No. 6380370

GENBEAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOLLEIC ACLD AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BUILDED FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEPERBRENCK. Christian
APPLICANT: DEPERBRENCK. Christian
APPLICANT: DEPERBRENCK.
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: DA Assessing DNA Methylation
FILER EMERBRENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR PRILING DATE: 2000-04-06
FRIOR PRILING DATE: 2000-04-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR APPLICATION NUMBER: DE 10033529.7
FRIOR APPLICATION NUMBER: DE 10033529.7
FRIOR SEQ ID NOS: 98
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAATCGCAAGAAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   803 AACCAATTGAAACAGAGCAATTACTAGAAATCATTGACGTTTTATCAGAAGAGAAAAT 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 CAATTATGTAAGATTACATTGTTTAGTAAAAATCAATTTCTAGAGTCATAAAT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        863 TAATATCTGAAGCTGATCAGTATCAATTCCAAGTTTATACTATTCAGAATTGAAAAGTG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 ATCTACCICGTACAATIGITATAGAAACAACACAAATTTACTCAATGAAGATATTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.0%; Score 46.4; DB 4; Length 2448; Best Local Similarity 52.0%; Pred. No. 0.017; Matches 104; Conservative 0; Mismatches 96; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; CRGANISM: Staphylococcus epidermidis US-09-134-001C-777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     923 TGĆAAAACTTATACCGAATT 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GCCTAAATTAAAATTCTATT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-204-708-35/c
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2448
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: variable motif ATTTA or TTTTT
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LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 10-513-365 : polymorphic base A or G NAME/KEY: allele
LOCATION: 3802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : polymorphic base C or T
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JTHER INFORMATION: 10-511-62 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : polymorphic base A or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 10-512-36 : polymorphic base G or NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : insertion of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : deletion of C
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                                                                                                                                                                                                                                                                                                                                                                                       COCATION: 17555.20674
DTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
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CCCATION: 1182
CTHER INFRMATION: 10-508-245
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 10-509-284
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OTHER INFORMATION: 10-511-337
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OTHER INFORMATION: 10-513-262
NAME/KEY: allele
NAME/KEY: 311e1e
OTHER INFORMATION: 10-513-352
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OTHER INFORMATION: 10-343-231
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LOCATION: 1827
OTHER INFORMATION: 10-510-173
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STHER INFORMATION: 10-509-295
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THER INFORMATION: 10-512-318
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INFORMATION: 12-206-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: 10-508-191
NAME/KEY: exon. 12254...12340
COTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854...13023
CITHER INFORMATION
                                                                                                                                  NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
                                                                                                                                                                                                                                                                                                                                LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                         LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
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LOCATION: 4062
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LOCATION: 2341
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LOCATION: 2832
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LOCATION: 2947
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INCATION: 8926
OTHER INFORMATION: 10-349-368: polymorphic base C or T NAME/KRY: allele
INCATION: 12171
OTHER INFORMATION: 10-350-72: polymorphic base C or T NAME/KRY: allele
INCATION: 123-73
OTHER INFORMATION: 10-350-332: polymorphic base C or T NAME/KRY: allele
INCATION: 13341
OTHER INFORMATION: 10-507-170: polymorphic base A or G NAME/KRY: allele
INCATION: 13492
OTHER INFORMATION: 10-507-321: polymorphic base A or G NAME/KRY: allele
INCATION: 13524
OTHER INFORMATION: 10-507-353: polymorphic base C or T NAME/KRY: allele
INCATION: 13536
INCATION: 13536
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
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OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8719
OTHER INFORMATION: 10-349-216 : deletion of CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 7668
LOCATION: 7668
LOCATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 10-347-74 : polymorphic base A or NAME/KEY: allele LOCATION: 6375 CTHER INFORMATION: 10-347-111 : polymorphic base G or NAME/KEY: allele LOCATION: 6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : polymorphic base A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 6467
CTHER INFORMATION: 10-347-203:
NAME/KEY: allele
LOCATION: 6484
CTHER INFORMATION: 10-347-220:
NAME/KEY: allele
LOCATION: 6534
CTHER INFORMATION: 10-347-271:
NAME/KEY: allele
                                                                                                                                                                                                                               OTHER INFORMATION: 10-346-263
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305
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LOCATION: 8785
OTHER INFORMATION: 10-349-224
NAME/KEY: allele
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THER INFORMATION: 10-347-165
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THER INFORMATION: 10-347-348
                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 6141
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GENERAL INFUGURATION:
GENERAL INFUGURATION:
GENERAL INFUGURATION:
APPLICANT: BIERING KAIT
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: DS/10/204,708
FRIOR APPLICATION NUMBER: PCT/FP01/03971
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR FILING DATE: 2000-06-30
FRIOR SEQ ID NOS: 98
LENGRAPH 6656
                                                                                                                                                                   54 ATTACTICTICTADATCATITCAGAGGATGAAAAAAAAAAAAAGCAAGAAAGCAAATATTTA 113
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                                                                                                                                                                                                                                                     5487 ATTGTTTTAAGATTTTTTAATCTCGTCAATGATTTTAAAATAAAAATCGATACATAATTT
                                                                                                                                                                                                                                                                                               174 TCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATTAAAATTCTATTTTT
                                                                                      Gaps
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                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-75
                                          Score 44.8; DB 1; Length 5852;
Pred. No. 0.073;
0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GGGACCATTAGAATGCGCGCTGCTCCATTTTTTATATAGAGATAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%; Score 44; DB 4; Length 6656; Best Local Similarity 49.6%; Pred. No. 0.13; Matches 113; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 75, Application US/10204708
Patent No. 6677731
                                       2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                       Query Match
Best Local Similarity 52.77
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         5607 TTTT 5610
                                                                                                                                                                                                                                                                                                                                                                                 234 CCTT 237
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GENERAL INFORMATION:
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US-07-867-106-2
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                                                                                                                                       11341 ATTTAATTTAATTAAATTAAATTAAATTAAGTTAAATTAATATTAAATTAAATTAAGTT 11282
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                                                                                                                                                                            97 AGAAAGCAAATATTTTAAATGAATGATACAATATACAAATTTAATTTACACAATTATGTAA
                                                                                               Gaps
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STREET: One Liberty Place 46th Ploor
CITY: Philadelphia
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APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Reith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
               Score 46; DB 4; Length 20674;
Pred. No. 0.068;
                                                       0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: FEERNCE/COCKET NUMBER: 35,134
REGISTRATION NUMBER: RICE-0002
TELEPHONE: 215,568-1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
             2.8%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5852 base pairs
                                                     Matches 106; Conservative
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2378..5038
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MEDIUM TYPE: Floppy
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STRANDEDNESS: sing
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                                 Best Local Similarity
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FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                       217
             Query Match
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CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.8%;
Matches 99; Conservative (
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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LOCATION: (28222)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (28257). (28258)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
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LENGTH: 1664976
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                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-204-708-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 TACATGIGALAAATTITATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAAAAA
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             1138 AATATAATTAAAATCTATTACTCACCAAATCTTTCAATATACTAAAAT 1091
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47.8%; Pred. No. 0.74;
tive 0; Mismatches 140; Indels 0
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                                                                                                                                                                                  APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Galcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILLE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Patent No. 6410712
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Matches 128; Conservative
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                                                                                                                                                                       GENERAL INFORMATION:
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US-10-204-708-74/c
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                                                                                   SULT 9
-09-426-290-1/a
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NAME/KEY:
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LOCATION:
NAME/KEY:
LOCATION:
NAME/KEY:
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APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERRENCE: PR275
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR PILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                               ó
                                                                                                                                                                                                                  83 AAAAAAAATCGCAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATT 142
                                                                                                                                                                                                                                                                 143 ACACAATTATGTAAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAAT 202
                                                                                                                                                                                                                                                                                                                                                      4854 AAATAAACATATTATTTAACAATAAACTACCTTATTTAAAACTATTTACTCATTTATTTC
                                                                                                                               Gaps
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                  Length 5152;
                                                                                                                               Indels
                                                                             Score 43.8; DB 4;
Pred. No. 0.13;
0; Mismatches 92;
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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or g or ör ö or or or or or ö or or NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc feature or t, α, ΰ ú NANE/KEY: misc feature LOCATION: (1664854)..(1664855) OTHER INFORMATION: n equals a, t, c, ບັ NAME/KEY: misc\_feature LOCATION: (871619) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc\_feature LOCATION: (1084830) .. (1084830) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc\_feature LOCATION: (855539)..(855539) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (113881)..(1119881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1349491) ...(1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1470091) ...(1470091)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (674435)..(674435) OTHER INFORMATION: n equals a, LOCATION: (657081)...(657081)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (657203)...(657203) NAME/KEY: misc feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, LOCATION: (779576)..(779676) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature NAME/KEY: misc feature LOCATION: (1096846)..(1096846) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature\_ LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1602912)..(1602912) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, LOCATION: (1603734)..(1603734) OTHER INFORMATION: n equals a, NAME/KEY: misc feature NAME/KEY: misc feature

or g

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AND AMINO ACID SEQUENCES RELATING TO PABECTUM FOR DIAGNOSTICS AND THERAPEUTICS
3571 ACCTAAAAACAAAAACAATTACGTTTTTACATTTTAAAATTTACTATTTAAATATAAA 3512
                                                                                                               101 AGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTATGTAAGATT 160
                                                            408 ATTTAGTAGTAGTATTTACAATTAAAGAAGGTAAAAATATAGAAGAAAATGATAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and David Bush
AND AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...1296
SEQUENCE DESCRIPTION: SEQ ID NO: 3402:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
RRGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3402, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1296 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3402:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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ilarity 49.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 112; Conserva
                                                                                                                                                                                                                                       3451 AATAA 3447
                                                                                                                                                                                 242 AAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-107-532A-3402
                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-107-532A-3402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                  182
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                                                                                                                                                                                                                                          159284 талаасатасалалалалаласаластсаталаттстстталалаталаласттталалтт 159343
                                                                                                                                                                                                                                                                                                                                                      159404 TCTTAAAAATCCGAAAGATTTCTAAAACCTGTTCGCTATGCTCACAAGAAGCAAGAATT 159463
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                                                                                                                                                                                                                                                                                                                                                                                                                     155 AAGATTACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 CAAGAAAGCAAATATTTTAAATGAATGATGCAATATACAAATTTAATTACACAATTATGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATTCTATTCTATTTTCCTTAAGAAAAAAAAACAGCCCATTAAGGGACCATTAGAATG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AATTCACGGCTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTC 61
                                                                                                                                                                                    Gaps
                                                                                                                              Gaps
                                                                     Length 1664976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159524 TATACATCACTATTTGTCATTAATGATAATGATAAATTACTGGTGAC 159570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 CGCGCTGCTCCATTTTTTATATAGAGATATGAGTTGTTGCTCAC 321
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                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 126;
                                                                                                                           0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43.4; DB 4;
Pred. No. 0.18;
                                                                  Score 43.8; DB 4;
Pred. No. 2.9;
                                                                     2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.6
Matches 119; Conservative
                                                                                                                              Conservative
                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-204-708-87/c
                                                                                                                              Matches 135;
            US-08-916-421B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
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                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                 Sequence 3111, Application US/09134000C

Sequence 3111, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCOCCUS FACCALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PRIOR DATE: 1997-08-15
161 ACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATTAAAATT 220
                                                                                                                     528 TGATCTTGAATTACTAGATATTGAAAAAGTGGAAAAATAAAAAGTCATAAATTTAAAAT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 ACATIGITIAGITICATAGAAATCAATTICTAGAGTCATAATAATGCCTAAATTAAAATT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 TGATCTTGAATTACTAGATATTGAAAAAGTGGAAAAATAAAAAGTCATAAATTTAAAAT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTAGTAGTAGTATTTACAATTAAAGAAGGTAAAAATTAGAAGAAAATGATAAGAA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 TTCAATTATTGTTCATGAAGAATTTGCTAAACAAACAATCTAAAATTAGGTGATGAAGT
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Sequence 2, Application US/07867106

Sequence 2, Application US/07867106

Patent No. 5389526

APPLICANT: Slade, Martin B

APPLICANT: Chang, Andy C M

APPLICANT: Williams, Keith L

TITLE OF INVENTION: Improved Plasmid Vectors for Cellular

TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSE: Moodcock Washburn Kurtz Mackiewicz & No. 5389526ris

STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                   221 CTATTCTATTTTCCTTAAGAAAAAAAAACAGCCCATTAAGGGACCAT 267
                                                                                                                                                                                                                  588 TATAGGGATCTTTTCTGGTAAAAACAGGAAACATATACAGGATTAT 634
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Pred. No. 0.099;
0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.6%;
Best Local Similarity 49.3%;
Matches 112; Conservative C
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ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                               US-09-134-000C-3111
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83 AAAAAAAATCGCAAGAAAGCAAATTTTTAAATGAATGATGCAATATACAAATTTAATT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1730 AATGAATGTCATCAAATAGTATTTTTAACATTTTTT 1696
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Job time : 150 secs
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 5852 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single "nobology: linear foenominate of the second strands of t
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Floppy disk
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LOCATION:
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FEATURE:
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Sequence 230, App
Sequence 236, App
Sequence 276, App
Sequence 276, App
Sequence 2147, Ap
Sequence 498, App
Sequence 187, App
Sequence 1179, Ap
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Sequence 7252, Ap
Sequence 13779, A
Sequence 3295, Ap
                                                                                                                                                   2, 2004, 09:38:09; Search time 785 Seconds (without alignments) 10498.497 Million cell updates/sec
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'cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

'cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

'cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*

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'cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

'cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

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'cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

'cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

'cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-425-114-7252

3 US-10-425-114-7252

3 US-10-425-114-1379

3 US-10-425-114-1379

5 US-10-425-114-1379

5 US-10-311-455-230

15 US-10-311-455-276

15 US-10-311-455-2147

17 US-10-311-455-2147

18 US-10-221-714A-498

19 US-10-311-455-1179

15 US-10-314-455-1179

15 US-10-314-455-1179

15 US-10-240-485-105

15 US-10-239-676-206
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                       sw model
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                                                                                               nucleic search, using
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Maximum DB seq length: 200000000
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Match Length DB
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1658
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3.1 6012
3.1 16265
3.1 113516
3.1 17280
3.0 1134
3.0 15767
3.0 15767
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Perfect score:
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                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                           Run on:
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Sequence 2080, Ap	Sequence 304, App				Sequence 142028,	Sequence 1, Appli	Sequence 21828, A	13	80	30	43	57,	53,	e 73	21	87	12		96	82	185	199	Sequence 36, Appl		Sequence 2, Appli			Sequence 543, App		
US-10-311-455-2080	US-10-240-453-304	US-10-027-632-104828	US-10-027-632-104828	US-10-027-632-142028	US-10-027-632-142028	US-10-312-841-1	US-10-437-963-21828	US-10-240-485-137	US-10-204-708-80	US-10-240-453-302	US-10-221-613-43	US-09-772-134B-57	JS-09-772-134B-53	US-10-311-455-736	US-10-311-455-2136	US-10-311-455-875	US-10-311-455-1248	US-10-312-841-2	US-10-239-676-76	US-10-240-453-82	US-10-239-676-185	US-10-311-455-1995	US-10-433-793-36	US-10-312-841-1	US-10-433-793-2	-10-311-	US-10-172-086-17	US-10-311-455-543	0-311-50	US-10-311-455-2148
15	15	13	16	13	16	15	17		15			•		15	15	15	15	12	15	15	15	S.	17	15	17	15	15	15	17	15
17142	17142	653	653	778	778	3673778	591	14551	8961	8961	5891	632	736	5313	5768	7276	13038	3673778	6053	6053	7657	7657	33053	3673778	5499	9963	18997	18997	18997	113515
3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	•		m.	m	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9
				49.6		49.6	49.4	49.4	48.8		48.6	48.4	٠,	48.2	48.2		48.2	48.2	48	48	48	48	48					ζ.	47.6	47.6
15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	
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## ALIGNMENTS

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Sequence 1, Application US/10732721
Publication No. US20040163144A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Thereof
FILLE OF INVENTION: Thereof
FILLE OF INVENTION: Thereof
FILLE REPERENCE: 38-15 (52826) A
CURRENT APPLICATION NUMBER: US/10/732,721
CURRENT FILING DATE: 2003-12-10
PRIOR PAPLICATION NUMBER: US/60/434,242
PRIOR FILING DATE: 2002-12-18
NUMBER: OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 1658; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1658
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US-10-732-721-1
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US-10-221-613-236/c
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                            APPLICANT: Screen, Seven E
APPLICANT: Screen, Seven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stou, Yihua
APPLICANT: Stou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: 
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99.0%; Pred. No. 1.4e-13;
tive 0; Mismatches 1;
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US-10-425-114-3295
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Best Local Similarity 99.0°
Matches 98; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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; Sequence 230, Application US/10311455 ; Publication No. US20030143606A1

US-10-311-455-230/c

RESULT 5

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APPLICANT: OLEK, Alexander
APPLICANT: DIERDRENGCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: cytosine methylation
FILE REPERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10012529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 230
LENGTH: 7498
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REPERENCE: 5013.1004
CURRENT APPLICATION NUMBER: US/10/221,613
CURRENT FILING DATE: 2002-09-13
FRICR APPLICATION NUMBER: PCT/EP01/02945
DE 100194058.8
DE 10019173.8
DE 1001943826.1
DE 1001943826.1
FRICR FILING DATE: 2001-03-15
2000-03-15
2000-04-06
2000-06-30
2000-06-30
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al Similarity 49.4%;
133; Conservative
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Best Local Similarity
Matches 94; Conserva
Best Local Similarity
Matches 133; Conserv
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US-10-311-455-2147/c
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APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTIONS A No. US2002019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
SOFTWARE: PACENTIN VOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TCAATTTCTAGAGTCATAATAATGCCTAAATTAAAATTCTATTCTATTTTTTCCTTAAGAA
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                                                                                                                                                                                          Gaps
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                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-613-236
                                                                                                                                                        Length 6012;
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                                                                                                                                                      Score 52.2; DB 13;
Pred. No. 0.1;
0; Mismatches 128;
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Patent No. US20020019995A1
GENERAL INFORMATION:
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                                                                                                                                                            3.1%;
50.2%;
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                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                        Query Match
Best Local Similarity 50.2;
Matches 129; Conservative
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       NUMBER OF SEQ ID NOS:
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                        SEQ ID NO 236
LENGTH: 6012
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NAME/KEY:
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NAME/KEY:
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Length 6265;

3.1%; Score 51.4; DB 9;

Query Match

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Sequence 276, Application US/10311455
; Sequence 276, Application US/10311455
; Sequence 276, Application No. US20030143606A1
; GENERAL INFORMATION:
    APPLICANT: OLER, Alexander
; APPLICANT: OLER, Alexander
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: Cytosine methylation
; TITLE OF INVENTION: Cytosine methylation
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR PILING DATE: 2000.06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NOS: 2424
; SEQ ID NO 276
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                                                                                                                                                                  84 AAAAAAATCGCAAGAAAGCAAATTTTTAAATGAATGATGCAATATACAAATTTAATTA
                                                                  24 TCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGA
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Pred. No. 0.16;
0; Mismatches 136; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3485 AAAATATAAAAATAATTCAACTTTTT 3457
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98 GAAAGCAAATTTTTAAATGAATGATGCAATATACAAATTTACACAATTATGTAAG 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Neutron, Applicant Applicant: Neutron, Applicant: Neutron, Applicant: Applicant: Applicant: Cafferkey, Robert Applicant: Sun, Yongming Applicant: Sun, Yongming Applicant: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific TITLE OF INVENTION: Genes and Proteins TITLE OF INVENTION: Genes and Proteins CURRENT Applicanton NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR FILING DATE: 2001-02-13
NUMBER: OF SEQ ID NOS: 295
SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                 11 CTCACAATACCAGTCATCTACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCA
                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-714A-498
                                                                                                                                                                    DB 13; Length 17280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/10074475
Publication No. US2003009289BA1
         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-074-475-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                        TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NOS: 2424

LENGTH: 113515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2147
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APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with

TITLE OF INVENTION: tumor suppressor genes and oncogenes

FILE REFERENCE: 5013.1005

CURRENT APPLICATION NUMBER: US/10/221,714A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 50.8; DB 15; larity 51.8%; Pred. No. 1.7; Conservative 0; Mismatches 107;
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PRIOR PILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: PCT/E201/02955
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 1001973.8
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 498, Application US/10221714A
Publication No. US20040048254A1
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 115; Conserval
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APPLICANT: OLEX, Alexander
APPLICANT: OLEX, Christian
AFPLICANT: DIEDENBROCK, Christian
AFPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10032529.7
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                             Length 15767;
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Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 136;
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PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-09-01 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 206, Application US/10239676; Publication No. US20030082609A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 49.3%
Matches 132; Conservative
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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 206
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ORGANISM: Artificial
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Best Local Similarity
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                                                                                                                                                                             SEQ ID NO 105
LENGTH: 15767
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.104
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
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     209 CAGACTACTAAATTTGGCATAAGAATAATTCTTTTAAAATGCAACATA 256
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Publication No. US20030148327A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Metastasis
FILE REFREENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
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49.3%; Pred. No. 0.55;
tive 0; Mismatches 136;
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                                                                                                                           Sequence 1179, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1179
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les 132; Conserv
                                                                              RESULT 12
US-10-311-455-1179
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US-10-240-485-105
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Matches
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RESULT 15
US-10-311-455-2080/c
is Sequence 2080, Application US/10311455
is Publication No. US20030143606A1
is GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
is APPLICANT: DLEK, Alexander
is APPLICANT: DLEK, Alexander
is APPLICANT: DLEK, Nurt
is TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
is TITLE OF INVENTION: Cytosine methylation
is TITLE OF INVENTION: Cytosine methylation
is TITLE OF INVENTION: Cytosine methylation
is TITLE OF INVENTION: Cytosine methylation
is TITLE OF INVENTION: Data: 2002-12-16
is PRIOR APPLICATION NUMBER: DC17/EP01/07537
is PRIOR FILING DATE: 2001-06-30
is PRIOR FILING DATE: 2000-06-30
is PRIOR FILING DATE: 2000-06-30
is PRIOR FILING DATE: 2000-09-01
is NUMBER OF SEQ ID NOS: 2424
is SEQ ID NOS: 2424
                                                                          9510 ATATCACAAATATCTATAAAATAACTTTAAAAACAAAACTTTTATTCCAAAAATCTCCA 9451
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          0;
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Pred. No. 0.65;
0; Mismatches 118; Indels 0;
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    0; Mismatches 118; Indels
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Job time : 792 secs
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.6%;
Matches 121; Conservative (
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Maximum Match 100%
Listing first 45 summaries
                              nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Best Local Similarity 100.0%; Pred. No. 0; Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GAATTCACGGCTCACAATACCAGTCATCTACATGTGATAAT	CACGGCICACAAIACCAGICAICIACAIGAAAAIIIIAAAGIIAGAIIACII	CATTICAGAGGATGAAAAAAAAATGCGCAAGAAAGCAAATATITITAAATGAAT 12:	zagaggatgaaaaaaaatcgcaagaaagcaaatatttaaat	CACAATTATGTAAGATTACATTGTTTAGTTTCA	121 C21 C22 C22 C22 C22 C22 C22 C22 C22	C CERTIFICATION OF THE STATE OF	181 AATCAATTTCTAGAGTCATAAJAATGCCTAAATTAAAATTCTATTCT	TAGAGTCATAATAATGCCTAAATTAAAATTCATTTTTTCCT	GGACCATTAGAATGCGCGCTGCTCCATTTTTAT			301 GAGATATGAGTGTTGCTCACTAGGCCACTCCACCTCGCATGCGTGTTCTTATTACATG 360	stracticactadeccacticacticacarecerdiricitral	BAGCCGCTTTTGCATTAAGGGTCTAGAGATGTACGAGTGCAA	SCATTAAGGGTCTAGAGATGTACGAGTGCAACGCTTC	いいしょ みたい かいかい かんかい きんかい きんしゅん かんしゅん かんしゅん かんしゅん かんしゅん しんしゅん しんしゅん しんしゅん しんしゅん しんしゅん しんしんしん しんしんしん しんしんしん しんしんしんしん しんしんしん しんしんしん しんしんしんしん しんしん しんしんしん しんしんしん しんしんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしん しんしんしん しんしん しんしんしん しんしんしん しんしんしん しんしん しんしん しんしん しんしん しんしん しんしんしん しんしんしんしん しんしんしんしん しんしんしんしんしん しんしんしんしんしん しんしんしん しんしんしん しんしんしんしんしん しんしんしん しん		3AGTAATTTTTTTTAATGCACGGAGGCGCTTTGTATTCCT	SCCCGTGCTTCGTGTACGGC		CCTGCCCACCGTGATGGCAAGGCTTGCTTGCTTGCGTC		7.5.1.0.1.0.1.0.1.0.1.0.1.0.1.0.1.0.1.0.1	AGGACGAGGTTGAAGCTACGGCGGTGCTTGCTTGCCTGCGCGCGTGCTAGCACGACCAC	TACGGCGGTGGCTGCCTGCGCGCGTGCTAGCACGCGAC 6	61 GACGTCGACGCTGATGCTACTTATTGTTTTTGTTTTCTCTGTGCTTGCGATG	CrcrerectreceAre 72	GIGIAICTCAIGIGAITGAICGACGIGIGICGGCGAITICAA 78	stótatétéatgattaatcaacetetetece	CACATGTGCATCCCCATCGACTTCGTGTCGGCGATA	TGTGCATCCCCATCGACTTCGTGTCGGCGATAAAI	SCITITCATGIATGAGATAGAGAGGAAGGAATAATA	TTCATGTATGTGCTTGAATAGAGGAAAGAAGAATAATAATTACATAAAA	CTTAATACCTTTTGCTCGATCTCCTTAGTAGAGCCA	01 GAGTICAACAICTITCTIAAIACCIITIGCICCAICCCITAGIAGAGCCACGIG	CGAGTGTAGTCCAAGGCTGCTTAACTGAA	CGTGTTAAGAACCCTTGTTACCGAGTGTAGTCCAAGGCTGCTTAA	1021 TAGAACACAAGGAGACAAGAGTGTAGAAGAACTGATTGTTTGT	
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	100 US-60-434-242-1	110 US-60-531-039-16 26 US-09-620-111B-7324	18 US-09-304-517A-40406	42 US-09-985-678-40406	35 US-09-865-439A-30469 76 US-60-207-458-74766	35 US-09-865-439A-27134	/6 US-6U-2U/-458-/1431 46 US-10-155-881-37309	51 US-10-425-114-7252	51 US-1U-425-114A-7252 88 US-60-312-544-973	27 US-09-654-617-273716 29 IIS-09-684-016-273716	51 US-10-425-114-13779	51 US-10-425-114A-13//9 18 US-09-304-517A-78600	19 US-09-371-146A-78600	42 US-09-985-678-78600	18 US-09-304-51/A-395// 19 US-09-371-146A-39577	42 US-09-985-678-39577 35 US-09-865-439A-48132	76 US-60-207-458-92395	18 US-09-303-031A-3934 18 US-09-304-517A-57027	19 US-09-371-146A-57027	36 US-09-894-949A-3994	42 US-09-985-678-57027 18 US-09-304-517A-79013	19 US-09-371-146A-79013 24 US-09-565-306-1774	42 US-09-985-678-79013	35 US-09-865-439A-43255 76 US-60-207-458-87528	35 US-09-865-439A-31938 76 US-60-207-458-76235	35 US-09-865-439A-44537	18 US-09-304-517A-39265 19 US-09-371-146A-39265		ALIGNMENTS			60434242	LC Specific		t: US/60/434,242 12-18	13.2				100.0%; Score 1658; DB 100;
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Db	138			OY 1621 CCGAGCTCGCCAGTTTTGCTCGTTAGTTTGGGACGGCG 1658	RESULT 2 US-60-531-039-16 US-60-531-039-16 ; Sequence 16, Application US/60531039 ; GENERAL INFORMATION: ; APPLICANT: Zheng, Wei ; APPLICANT: Savidge, Beth ; APPLICANT: Savage, Thomas ; APPLICANT: Chaudhuri, Sumita	; TITLE OF INVENTION: Materials and Methods for the Modulation of D-type Cyclins in ; TITLE OF INVENTION: Plants ; FILE REFERENCE: REN-01-083 ; FILE REFERENCE: REN-01-083 ; CURRENT APPLICATION NUMBER: 05/60/531,039 ; CHERENCE APPLICATION NUMBER: 05/60/531,039 ; CHERENCE APPLICATION NUMBER: 05/60/531,039 ; CHERENCE APPLICATION NUMBER: 05/60/531,039	CORRENT FILLING DATE: 2003-12-19  COFTWARE: Patentin version 3.2  SOPIWAR: Patentin version 3.2  The control of the control of	; TYPE: DNA ; ORGANISM: Zea mays US-60-531-039-16	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TTTTATAGTTAGATTACTT 60	

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99.0%; Pred. No. 3.9e-12;
live 0; Mismatches 1;
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Best Local Similarity 99.0%; Pred. No. 3.9e-12;
Matches 100; Conservative 0; Mismatches 1;
                                                                                                               Annotated Plant Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40466, Application US/09371146A; GENERAL INFORMATION:
APPLICANT: Chelkh, Nordine; APPLICANT: Chelkh, Uningdong; TITLE OF INVENTION: ANNOTATED PLANT GENES; FILE REFERENCE: 38-21(15097); CURRENT APPLICATION UNDHER: US/09/371,146A; CURRENT FILING DATE: 1999-08-09; PRIOR APPLICATION NUMBER: US 09/304,517; PRIOR FILING DATE: 1999-05-06; NUMBER OF SEQ ID NOS: 294310; SEQ ID NO 40406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cheikh, Nordine
APPLICANT: Cheikh, Nordine
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517.255/38-21(15097)F
CURRENT APPLICATION NUMBER: US/09/985,678
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
                                                                                                               CURRENT APPLICATION NUMBER: 1509/304,517A CURRENT FILING DATE: 1999-05-06 NUMBER OF SEQ ID NOS: 295529 SEQ ID NO 40406 LENGTH: 308
            Seguence 40406, Application US/09304517A GENERAL INFORMATION:
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$2.09-985-678-40406

; Sequence 40406, Application US/09985678
; GENERAL INFORMATION:
                                                             Cheikh, Nordine
Liu, Jingdong
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Best Local Similarity 99.0
Matches 100; Conservative
                                                             APPLICANT: Chu, Jing
APPLICANT: Liu, Jing
TITLE OF INVENTION:
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Zea mays
US-09-371-146A-40406
                                                                                                                                                                                                                                                                                                        ; ORGANISM: Zea mays US-09-304-517A-40406
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                                                                                                                                                                                                                                                                                    TYPE: DNA
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1070P
CURRENT APPLICATION NUMBER: US/09/620,111B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
SEQ ID NO 7324
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                                                                                        1380
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                                              1201 TCCAGGCGCGGCGTGCTGCTTCAACTCCTTCCCTCCGCCTCCAGAGCGGATAAATACG
                                                                                                                                            1261 GGGTCTACGGTGCACGCGCACGCATGGTGCGCCGAGGGGCATCTCTGCCCGGGGAATGCG
                                                                                                                                                                        CGCAGGCCATCGCTCGACACGCACGTACGTGTCGCCCCCCGCGAGGCCTCCTCGCACGC
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99.1%; Pred. No. 1.2e-14;
iive 0; Mismatches 1;
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NAME/KEY: misc_feature

LOCATION: 1..385

OTHER INFORMATION: any n = a, g, c, t, un

NAME/KEY: misc_feature

LOCATION: 1..385

OTHER INFORMATION: Ceres Seq. ID 1339942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 111; Conserv
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RESULT 9
US-09-865-439A-27134
; Sequence 27134, Application US/09865439A
; GENERAL INFORMATION:
    APPLICANT: Bedgetron, Michael D
; APPLICANT: La Rosa, Thomas J.
    TILLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
    TILLE OF INVENTION: Plants
    TILLE REFERENCE: 38-21(51936)B
    CURRENT APPLICATION NUMBER: US/09/865,439A
    CURRENT FILING DATE: 2001-05-29
    PRIOR FILING DATE: 2000-05-30
    NUMBER OF SEQ ID NOS: 119126
    SEQ ID NO 27134
    LENGTH: 470
    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                               1553 GCAGCAACAGCCAACACCTAAACTAAAGAACAGTAGTAGTCCCTGTGTACGTCTAGCAAC 1612
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                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                    Query Match 5.9%; Score 98.4; DB 76; Best Local Similarity 99.0%; Pred. No. 7.3e-12; Matches 99; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(470)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3354-008-P1-K1-B11
                                                                                                                                                                                        ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3354-052-P1-K1-G5
US-60-207-458-74766
                          FILE REFERENCE: 38-21 (51936) A CURRENT APPLICATION NUMBER: US/60/207,458 CURRENT FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 152403 LENGTH: 396
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Conner, Timothy W.
Deikman, Jill
Hardeman, Kristine J.
La Rosa, Thomas J.
            TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 99; Conserve
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
Sequence 30469, Application US/09865439A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANTION: Plants
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT APPLICATION NUMBER: US/02/29
FRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 30469
LENGTH: 396
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                                                                                                                                                         6.0%; Score 99.4; DB 42; Length 308; 99.0%; Pred. No. 3.9e-12; ive 0; Mismatches 1; Indels 0
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US-09-865-439A-30469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Deskman, Jill
APPLICANT: Deskman, Jill
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ruan, Yijun G.
APPLICANT: Rush, Yijun G.
APPLICANT: Sammons, R. Douglas
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Xu, Kunsheng
APPLICANT: Xu, Nanfei
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 74766, Application US/60207458; GENERAL INFORMATION:
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Conner, Timothy W.
NUMBER OF SEQ ID NOS: 295529
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Best Local Similarity 99.0%
Matches 99, Conservative
                                                                                                                                                                                                    Matches 100; Conservative
                                                                                                                                                                                 Best Local Similarity
                                                                                      ; ORGANISM: Zea mays
US-09-985-678-40406
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ORGANISM: Zea mays
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                     SEQ ID NO 40406
LENGTH: 308
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                   TYPE: DNA
                                                                                                                                                            Query Match
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Sequence 7222. Application US/10425114A
; Sequence 7222. Application US/10425114A
; GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: ADAU, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: ADABSEA, Jack E
; APPLICANT: CAO, YONGWei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE REFERENCE: 38-21(5313) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7252
ILENGTH: 836
                   APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 2552
LENGTH: 836
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Pred. No. 9.8e-12;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 98.4; DB 51; Length 836; 99.0%; Pred. No. 9.8e-12; tive 0; Mismatches 1; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700623908_FLI
US-10-425-114A-7252
                                                                                                                                                                                                                                                                                                                                              ), OTHER INFORMATION: Clone ID: 700623908_FLI
US-10-425-114-7252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%;
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Best Local Similarity 99.0%
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Best Local Similarity 99.04
Matches 99; Conservative
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ORGANISM: Zea mays
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US-10-425-114A-7252
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US-60-312-544-973
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GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liuda L.
APPLICANT: Liuda L.
APPLICANT: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
TITLE OF INVENTION: US-10 (15300) J
CURRENT FILING DATE: 2002-05-22
CURRENT FILING DATE: 2002-05-22
SEQ ID NO 37309
LENGTH: 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1553 GCAGCAACAGCCAACACCTAAACTAAAGAACAGTAGTAGTCCCTGTGTACGTCTAGCAAC 1612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3354-008-P1-K1-B11
US-60-207-458-71431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 98.4; DB 76; 99.0%; Pred. No. 7.8e-12;
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                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
FILLE REPERENCE:
CURRENT APPLICATION NUBBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS:
LENGTH: 470
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                            Ruan, Yijun G.
Ruff, Thomas G.
Sammons, R. Douglas
Shukla, Hridayabhiranjan
Wu, Kunsheng
         Lalgudi, Raghunath V.
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Best Local Similarity 99.0'
Matches 99; Conservative
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Best Local Similarity 99.03
Matches 99; Conservative
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; ORGANISM: Zea mays
US-10-155-881-37309
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US-10-155-881-37309
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US-10-425-114-7252
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Holde, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdon B.
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(5272,544
CURRENT APPLICANTON VUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
LENGTH: 836
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5.9%; Score 98.4; DB 88; Length 836;
Best Local Similarity 99.0%; Pred. No. 9.8e-12;
Matches 99; Conservative 0; Mismatches 1; Indels 0
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APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38.21(15097)D
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 273716
LENGTH: 861
                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (108)..(449)
; OTHER INFORMATION: Clone ID: 700623908_FLI
US-60-312-544-973
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Job time : 4955 secs
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US-09-654-617-273716
; Sequence 273716, Application US/09654617
; GENERAL INFORMATION:
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Best Local Similarity 99.0°
Matches 98; Conservative
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ORGANISM: Zea mays
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; ORGANISM: Zea mays
US-09-654-617-273716
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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

2, 2004, 07:52:53 September . uo Run

3; Search time 2370 Seconds (without alignments) 2423.549 Million cell updates/sec

US-10-732-721-1 1658 Perfect score:

1 gaattcacggctcacaatac.....ctcgttagtttgggacggcg 1658 Scoring table: Sequence:

5837357 seqs, 1732150321 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Pending Patents NA New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/USO6\_NEW\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq2:\*

9: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq2:\*

9: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			æ				
Res	Result No.	Score	Query	Query Match Length	DB	ID	Description
!	1	1658	100.0	1658	7	US-10-732-721-1	Semience 1 Appli
O	7	109	9.9	9	9	US-10-425-115-68623	ì
Ö	М	101.6	6.1	528	9	US-10-425-115-47987	
	4	100.4	6.1	975	9	US-10-425-115-181022	
O	Ŋ	84.8	5.1	2211	9	US-10-425-115-82158	
	9	71.4	4.3	1034	9	US-10-425-115-181033	
	7	55	3.3	533	σ	US-60-579-062-32930	
υ	œ	50.6	3.1	17280	9	US-10-221-714B-498	
	σ	50.4	3.0	805	Q	US-60-579-062-23067	2306
U	10	48.8	2.9	207542	Ŋ	US-09-949-003C-4513	
υ	11	48.8	2.9	207542	9	US-10-893-315-148	148. 2
บ	12	48.8	2.9	207542	9	US-10-902-387-493	493.
υ	13	48.8	2.9	207557	S	US-09-949-003C-3956	3956.
υ	14	48.8	2.9	207557	9	US-10-893-315-134	134. A
υ	15	48.8	2.9	207557	9	US-10-902-387-465	465.
U	16	48.8	2.9	215927	σ	US-60-582-609-19505	19505
υ	17	48.8	2.9	228854	σ	US-60-548-091-5633	5633
υ	18	48.2	2.9	791	S	US-09-404-520B-13329	
	19	48	2.9	753	σ	US-60-579-062-40662	4
υ	20	47.2	2.8	1882	Н	PCT-US03-41761-40265	
υ	21	47.2	2.8	1882	Н	PCT-US03-41761-40265	
υ	22	47.2	2.8	1882	٦	PCT-US03-41766A-40265	
	23	47.2	2.8	6106	9	US-10-221-714B-152	152,
υ	24	47	2.8	688	σ	US-60-579-062-40503	

Sequence 777, App Sequence 360, App	Sequence 24705, A	Sequence 162, App	Sequence 513, App	4		Ŋ	Sequence 472, App				Sequence 8, Appli	Sequence 526, App	109,	Sequence 423, App	Sequence 265, App	488,	203,	3720.	
US-10-902-441-777 US-10-724-972A-360	US-60-579-062-24705	US-10-221-714B-162	US-10-221-714B-513	US-60-579-062-41308	US-10-482-823-3	US-10-482-823-5	US-10-221-714B-472	PCT-US03-41761-20202	PCT-US03-41761-20202	PCT-US03-41766A-20202	US-10-221-714B-8	US-10-221-714B-526	US-10-221-714B-109	US-10-221-714B-423	US-10-221-714B-265	US-10-221-714B-488	US-10-221-714B-203	US-10-918-711-3720	US-10-918-754-16803
9	σ	9	9	σ	9	9	9	Н	Н	Н	9	9	9	9	9	9	9	9	9
2448 2448	916	7040	61020	594	29993	29993	38342	900	909	900	3952	5371	7133	8711	8845	8883	12426	77504	77504
2.2	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	5.8	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7
46.4 46.4	46.2	46.2	46.2	46	45.8	45.8	45.8	45.6	45.6	45.6	45.4	45.4	45.4	45.2	45.2	45.2	45.2	45.2	45.2
25 26	27	c 28	c 29	30	c 31	32	33	c 34	c 35	36	c 37	ი 38	c 39	c 40	c 41	c 42	c 43	44	45

## ALIGNMENTS

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Sequence 1, Application US/10732721

Sequence 1, Application US/10732721

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Maize Embryo-Specific Promoter Compositions and Methods for Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION UNMER: US/10/732,721
CURRENT APPLICATION NUMBER: US/60/434,242
FRIGH APPLICATION NUMBER: US/60/434,242
FRIGH APPLICATION NUMBER: US/60/434,242
SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NO 1
LENGTH: 1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGTAATCATTTCAGAGGATGAAAAAAAATCGCAAGAAAGCAAATATTTTAAATGAAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1658; DB 7; Length 1658;
.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1658; Conserv
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
US-10-732-721-1
RESULT 1
US-10-732-721-1
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301 GAGATATGAGTTGTTGCTCACTCACTCCACCTCGCATGCGTGTTCTTTATTACATG 360

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TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Associated S. Thomas J. APPLICANT: La Avaic, David K. APPLICANT: Avaic, David K. APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwar Title OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-2.1(53.22) B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT PILING DATE: 2003-04-28 CURRENT FILING DATE: 2003-04-28 SEQ ID NO 181022 LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         984 ACCGAGTGTAGTCCCAA-GGCTGCTTAACTGAATAATAGTAGAACACAAGGAGACAAGAGT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1551 CAGCAGCAACACCCAACACTAAACTAAAGAACAGTAGTAGTAGTCCCTGTGTACGTCTAGCA 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                             129 ccririccrccarcrrcarrragaccaccrccarcaraaccrcrraacaaccccrrccr
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                     Query Match 6.1%; Score 101.6; DB 6; Length 528; Best Local Similarity 91.5%; Pred. No. 1.7e-15; Matches 118; Conservative 0; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 100.4; DB 6; Length 975; 99.0%; Pred. No. 4.5e-15; ative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: MRT4577_14376C.1
US-10-425-115-47987
                                                                                                                                                             LOCATION: (1)..(528)
OTHER INFORMATION: unsure at all n locations
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US-10-425-115-181022
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; Sequence 181022, Application US/10425115
; GENERAL INFORMATION:
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"Sequence 82158, Application US/10425115
"GENERAL INPORMATION:
"APPLICANT: La Rosa, Thomas J.
"APPLICANT: Zhou, Yihua
"APPLICANT: Cao, Yongwei
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 47987
LENGTH: 528
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                                                                 TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
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Best Local Similarity
Matches 101; Conserv
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ORGANISM: Zea mays
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 82158
LENGTH: 2211
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 181033
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                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 84.8; DB 6; 92.6%; Pred. No. 5.9e-11; trive 0; Mismatches 7;
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98.6%; Pred. No. 1.1e-07;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_174942C.1 US-10-425-115-82158
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GENERAL INFORMATION:
APPLICANT: Baum, James A
APPLICANT: Rovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1640 TCGTTAGTTTGGG 1652
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Best Local Similarity 98.61
Teles 72; Conservative
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Best Local Similarity 92.6
Matches 100; Conservative
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-60-579-062-23067
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    ; US-10-221-714B-498
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APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION WUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: PatentIn version 3.2
SREQ ID NO 32930
LENGTH: 533
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Sequence 498, Application US/10221714B

Sequence 498, Application US/10221714B

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: DEFENBROCK, Christian

APPLICANT: DEFENBROCK, Christian

APPLICANT: DEFENBROCK, Christian

TITLE OF INVENTION: Diagnosis of Diseases Associated with

TITLE OF INVENTION: Diagnosis of Diseases and oncogenes

FILE REFERENCE: 5013.1005

CURRENT APPLICATION NUMBER: US/10/221,714B

CURRENT PILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: DE 10013847.0

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                     Length 533;
                                                                                                                                                                                                                                                                                                                                     Score 55; DB 9; Length 533
Pred. No. 0.0011;
0; Mismatches 175; Indels
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                                                                                                                                                                                                                                                                  ORGANISM: Diabrotica virgifera
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                   Query Match 3.3%;
Best Local Similarity 47.8%;
Matches 160; Conservative
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150 TATGTAAGATTACATTGTTTAGTTTCATAGAAATCA-ATTTCTAGAGTCATAATAATGCC 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arroscrrraharhirarcharitrirhakoahrahiraccorrahirhirkoahra 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 TTÄÄCATATGCTTTATCTTTATATATATTATTATTTTTTATTTTTTATÄGCTTCTTTÄ 501
                                                                                                                                                                                                                                     98 GAAAGCAAATATTTAAATGAATGATGCAATATACAAATTTAATTACACAATTATGTAAG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 ACATGTGATAAATTTTATAGTTAGATTACTTCTTGTAATCATTTCAGAGGATGAAAAAA
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                                                                                                                                                                                                                                                                                                                            158 ATTACATIGITIAGITICATAGAAATCAATTICTAGAGICATAATAATGCCTAAATTAAA
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                            Length 17280;
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                                                                Score 50.6; DB 6; Length 1
Pred. No. 0.073;
0; Mismatches 104; Indels
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3.0%; Score 50.4; DB 9;
Best Local Similarity 46.6%; Pred. No. 0.02;
Matches 194; Conservative 0; Mismatches 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R.
APPLICANT: Roberts, James K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Diabrotica virgifera
                                                                  Query Match 3.1%;
Best Local Similarity 52.1%;
Matches 113; Conservative
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GRERAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOO786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT APPLICATION NUMBER: 60/231,397
PRIOR PILING DATE: 2004-07-19
PRIOR FILING DATE: 2004-09-08
NUMBER OF SEC ID NOS: 2172
SEC ID NO 148
LENGTH: 207542
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APPLICANT: VENTER:
APPLICANT: VENTER:
APPLICANT:
APPLICANT: VENTER:
APPLICANT: VENTER:
APPLICANT: VENTER:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPTD DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOOO787
CURRENT APPLICATION NUMBER: US/10/902,387
CURRENT FILING DATE: 2004-07-30
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SSECTIANDS OF SEQ ID NOS: 6404
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Pred. No. 0.65;
0; Mismatches 132; Indels
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       280 IGCICCATITITIAIAI 299
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// OTHER INFORMATION: n = A,T,C or G
US-10-893-315-148
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Best Local Similarity 49.2
Matches 128; Conservative
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                                                                                                                                    RESULT 11
US-10-893-315-148/c
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ORGANISM: Human
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LENGTH: 207542
TYPE: DNA
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
CURRENT ELIE REFERENCE: CLO00791
CURRENT APPLICATION NUMBER: US/09/949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,446
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
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CTCCACCTCGCATGCGTGTTTTATTACATGAAAAAATGAGCCGCTGCTTTTGCATTAA 388
                                                       561
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                                               502 TIACAATATACAITTAAATTATTTAAATTTAGTAATGATGATAATATTACTATTACAAAA
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                                                                                            389 GGGTCTAGAGATGTACGAGTGCAACGCTTCGTATTCACTGCACGAGTAATTTTTT
                                                                                                                                                 562 TTGTCTATCTACTAAAATATATACGTTTAATAAAGGAATTCGGCCACATTTTTTT
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10.09-949-003C-4513/c

1. Sequence 4513, Application US/09949003C

1. GENERAL INFORMATION:
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LOCATION: (158403)..(158422)
OTHER INFORMATION: n is a, c,
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OTHER INFORMATION: n is a, c,
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LOCATION: (2975)..(2994)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
LOCATION: (125952)..(12
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LOCATION: (18838). (189
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LOCATION: (33239)..(359
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LOCATION: (45489)..(459
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LENGTH: 2075
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APPLICANT: VENTER, J. Craig et al.

IITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND

TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOOO786

CURRENT APPLICATION NUMBER: US/10/893,315

CURRENT APPLICATION NUMBER: 60/231,397

PRIOR APPLICATION NUMBER: 60/231,397

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2172

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 134

LENGTH: 207557
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                                                                    Length 207557;
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                                                                                                                  Indels
                                                                                                                  132;
                                                                 Score 48.8; DB 5;
Pred. No. 0.65;
                                                                                                                  0; Mismatches
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  or
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OTHER INFORMATION: n = A,T,C or G
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                                                                      2.9%;
OTHER INFORMATION: n is a,
                                                                                            Best Local Similarity 49.2
Matches 128; Conservative
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ORGANISM: Human
       ; Orner US-09-949-003C-3956
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US-10-893-315-134/c
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                                                                      Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO0791
CURRENT APPLICATION NUMBER: US/09/949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,446
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168244 ACTATGCAATTTTTAATTTGCAGAATAAGAAAACAATAATGGTTTTCTTCACATGACCAA 168185
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                                                                                                                                                                   Score 48.8; DB 6; Pred. No. 0.65; 0; Mismatches 132;
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; Sequence 3956, Application US/09949003C
; GENERAL INFORMATION:
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                                                | NAME/KEY: misc_feature
| LCCATION: (1)...(207542)
| CTHER INFORMATION: n = A,T,C or G
US-10-902-387-493
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LOCATION: (125952)..(131289)
OTHER INFORMATION: n is a, C,
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OTHER INFORMATION: n is a,
FEATURE:
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LOCATION: (18838)..(18906)
OTHER INFORMATION: n is a,
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Best Local Similarity 49.2*
Matches 128; Conservative
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LOCATION: (33239)..(359
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LOCATION: (45489)
       ORGANISM: Human
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Oy 280 TGCTCCATTTTTATATATA 299

Db 168184 TGTTAATTTTATATATA 299

Db 168184 TGTTAATTTTATATATA 168165

RESULT 15

US-10-902-387-465/C

SGURDER LINCORMATION:
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: UNDERS. US/10/902,387

CURRENT APPLICATION NUMBER: US/10/902,387

CURRENT APPLICATION NUMBER: 60/231,399

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 6404

SOFTWARE: PASISEQ for Windows Version 4.0

SEQ ID NO 465

SEQ ID NO 465

NAME/KEY: misc feature

COCADION: (1)-..(207557)

OTHER INFORMATION: n = A,T,C or G

US-10-902-387-465

DOWETW MARCH

BEST LOCAL SIMILARITY 49.2%; Pred, No. 0.65; 122; Indels 0; Gaps 0;
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168304 İGAATATİTAATİTĞÇAAAATTTTAATAATATAĞATAÇAÇATİTTATÇTĞÇATATĞAÇAT 168245 168424 AGTATTTTACATGATTAGATGCTAAATATTAGCTTAAAATAAGAAAACTAAGTTAATA 168365 160 TACATTGTTTAGTTTCATAGAAATCAATTTCTAGAGTCATAATAATGCCTAAATTAAAAT 219 AAGCAAATATTTTAAATGAATGAATGCAATATACAAATTTAATTACACAATTATGTAAGAT 159 220 TCTATTCTATTTTTCTTTAAGAAAAAAAAAAAAGGCCCATTAAGGGACCATTAGAATGCGGGC 279 280 IGCICCATITITITATAT 299 100 g à qq qq à δ  $\delta$ ΩD ð

Search completed: September 2, 2004, 12:48:44 Job time : 2374 secs

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CC418961 PUEDX81TD
CG146202 PUJCV14TB
CG152000 PUIFT17TD
CG146205 PUJCV14TD
                                                                 September 2, 2004, 07:29:38; Search time 3928 Seconds (without alignments) 12604.760 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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CG151999 PUIFT17TB CG175932 PUFYZ51TB BG705097 PUCEL43TD CG041829 PUFWI17TB CC654144 OGUDXZ0TV CG118361 PUFWI43TB CG175933 PUFYZ51TD CG43184 ZMMBRC034 CG463184 ZMMBRC034 CG06594 PUFUD51TB CG14346 PUITU51TB CG1446 PUITU51TB CC443358 PUBMBC0TD BZ988278 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CC352433 PUBMBC0TD CCG52076 PUFDS9TD	CG062075 PUFPD96TB CG096596 PUFUD53TD CG096596 PUFUD53TD CG193725 PUFUD37TB CG193725 PUTD73TB CG07629 PUFUA37TB CG05005 PUFUA36TB CG05005 PUFUA36TB CG05006 PUFUA36TB CG06006	NA linear GSS 19-MAY-200 nomic clone ZMMBTa230M18, rta; Embryophyta; Tracheophyta ssida; Poales; Poaceae; PACCAD fea. ken.S., Utterback,T., n Miguel,P., Ma,J. and ,, MD 20850, USA
CG151999 CG175932 CG175932 CG518129 CC654144 CG118361 CG118361 CG113123 CG113123 CG124386 CG124386 CG124366 CG124366 CG124366 CG124366 CG12433	CGG62075 CGG96596 CGG193725 CGG193723 CGG96729 CGG97259 CGG97259 CGG50059 CGG50059 CGG50059 CGG50059 CGG50059 CGG50059 CGG50059 CGG11830 CGG5045 CGG11830 CG	ALIGNMENT 779 bp 1 Zea mays 1. Zea mays 1. Zea mays 1. Zea mays 2.
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GAGTGTAGTCCAA-GGCTGCTTAACTGAATAATAGTAGAACACAAGGAGACAAAGGAGTGTA 1045
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                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Mitclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
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                                                                                                                                                                                                                         Unpublished (2003)
Other GSSs: PUJCV14TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, 1
Tel: 301-838-5443
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/strain="B73"
/db xref="taxon:4577"
/clone="ZMMBTa0639C04"
/clone lib="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site 1: Bc
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 survey sequence
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                                                                                                                                                                                            Length 779;
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                                               /moi_type="genomic DNA"
/strain="BAT"
/db xref="taxon:4577"
/clone="zmMBTa230M18"
/clone=lib="ZM.0.6.1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: Bc
CoT selected genomic DNA library"
                                                                                                                                                                                                                                 10;
                                                                                                                                                                                          Score 751; DB 28;
Pred. No. 1.4e-157;
0; Mismatches 10;
                1 779
/organism="Zea mays"
 Location/Qualifiers
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il Similarity 98.6%;
768; Conservative
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CG146202 754 bp DNA linear GSS 21-AUG-2003 PUJCV14TB ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMMBTa0633C04,

RESULT 2 CG146202/c LOCUS DEFINITION

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                                                                            548 ATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGGGGGATAAATCTGCTAGGG
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                                                      781 ATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGGCGATAAATCTGCTAGGG
                                                                                                                                    248 GCTCTCCAAAGGTTACATGATATAGGGGATCTTCTCTCTTTATTATAGACAAAACTAGGGTT
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           Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
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Unpublished (2003)
Other GSSs: PUJCV14TB
Contact: Cathy Whitelaw
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                                                                                                              CCTGGCGCGCGCGCGTGCCGCGTCTCCCCACCGGACGGCTATAAAAAGGCGGCGCC 1521
                                                                                                                                                                       ACCTGATCCTCCATCTCACAAGCAAGCAGCAGCAACAGCCAACACCTAAAAGA 1581
                                                                                                                                                                                                                                                                                                                                              CG152000 728 bp DNA linear GSS 21-AUG-2003 PUIFT17TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0573C10,
                                                                 214 GGGACCTIGCAATICGTCCGCGTCGGTGCACGTCCCTGGCCCCGGCTTGCCGGCTTTGC 155
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Peprantophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 728)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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/clone lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: BcoRI; 0.6-1.0 kb }
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contract: Cathy Whitelaw
TIGR
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TO SHE Can Contex Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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/strain="B73"
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Unpublished (2003)
Other GSSs: PUIFT17TB
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Seq primer: TF
Class: sheared ends.
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1315 CG146205
PUJCY14TD ZM 0.6\_1.0 KB Zea mays genomic clone ZMMBTa0639C04,
genomic survey sequence.
CG146205.1 GI:34036988 TICCAGGCGCGGTCGTGCTTCAACTCCTTCCCTCCGCCTCCAGAGCGG----ATAA 1255 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Pagerantophyta; Pagerantophyta; Dagera, Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 938)

Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. σ 68 ATACGGGGTCTACGGTGCACGCGCACGCATGCGTGCGCCGAGGGCATCTCTGCCCGGGGA 1256 ATACGGGGTCTACGGTGCACGCACGCATGGTGCGCCGAGGGGCCATCTCTGCCCGGGGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                    EcoRI; 0.6-1.0 kb
                                                      1 (bases 1 to 498)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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                                                                                                                                                                                           20850, USA
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                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4577"
/clone="xxwBTa0573C10"
/clone lib="zM_0.6_1.0 KB"
/note="Vector: pCR4_TOPO; Site_1:
CoT selected genomic DNA_library"
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                                                                                                                                                                                         9712 Medical Center Drive, Rockville,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
Location/Qualifiers
                                                                                                  Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUIFT17TD
Contact: Cathy Whitelaw
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/organism="Zea
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ilarity 99.4%;
Conservative
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495; Conserv
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Best Local S:
Matches 495,
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 ORGANISM
                                                         REFERENCE
AUTHORS
                                                                                                                 TITLE
JOURNAL
COMMENT
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PUIFT17TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0573Cl0, genomic survey sequence.
CG151999
CG151999.1 GI:34042782
GSS.
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                                                                                                        EcoRI; 0.6-1.0 kb high
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                                                                                                                                                                Length 938;
                                                                                                                                                                                              Indels
            /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db xref="taxon:4577"
/clone="ZMMBTa0639C04"
/clone lib="ZM,0.64"
/note="Vector: pCR4-TOF0; Site_1: Bc
CoT selected genomic DNA library"
                                                                                                                                                                40.7%; Score 674; DB 29;
llarity 98.3%; Pred. No. 2.5e-140;
Conservative 0; Mismatches 10;
                                                                                                                                                                                Similarity
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Matches 702;
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                                                                                                                                                                   Query Match
    source
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CG151999
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KEYWORDS
SOURCE
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CTCTCTATTTATAGAC-AAAACTAGGGTTTCAGGCATATGGGCCACATAGGCCTTCCTGG 1170
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                                                                          551 GACTGATTCTTATTACTGTATGGTGCTGTTGTCC-CAGGTTACATGATATGGGGATCTC 609
                                                                                                                                                                          699
                491 AGTCCAAGGACTCTTTAACTGAATAATAGTAGAACACAAGGAGACAAGAGTGTAGAGAGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                         BZ705097 949 bp DNA linear GSS 19-F
PUCEL43TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa127G13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 949;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, 'Tel: 301-838-5843
Fax: 301-838-0208
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="Bn3"
/db_xref="taxon:4577"
/clone="xear = 12M 0.6 1.0 / Clone lib="ZM 0.6 1.0 / Clone lib="ZM 0.6 1.0 / Clone lib="ZM 0.6 1.0 / Clone lib="yextrain"
/clone lib="XM 0.6 1.0 / Clone lib="yextrain"
/clone lib="XM 0.6 1.0 / Clone lib="yextrain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.5%; Score 373; DB 28; 97.3%; Pred. No. 7.3e-73; ive 0; Mismatches 10;
                                                                                                                                                                                                                CCCAAGAAAGGTTTCTTAACACTACCATCTT 1201
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                                                                                                                                                                                                                                         CCCAATAAAGGTTTCTTAACACGCCCAACCT
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence.
BZ705097
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962 bp DNA linear GSS 21-AUG-2003
PUFYZ51TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa0765106,
GG175932
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                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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clade; Panicoideae; Andropogoneae; Zea.
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/clone="ZMMBTa0765106"
/clone="lb="ZM_0.6_1.0 KB"
/note="Weetor: pCR4_TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
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/strain="B73"
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/organism="Zea mays"
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Unpublished (2003)
Other GSSs: PUFYZ51TD
Contact: Cathy Whitelaw
TIGR
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                                                                                                          CG175932.1 GI:34066730
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Class: sheared ends.
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CC654144 373 bp DNA linear GSS 19-JUN-2003 OGUDK20TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0415C15, genomic survey sequence.
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Zea mays

Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;

Eukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae, PACCAD

Clade, Panicoideae, Andropogoneae; Zea.

1 (bases I to 373)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
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CCTTAGTAGAGCCACGTGCGTGATAACGTGTTAAGAACCCCTTGTTACCGAGTGTAGTCC
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/strain="B13"
/db xref="taxon:4577"
/clone="ZMMBMa0415c15"
/clone lib="ZM 07 1.5 KB"
/note="Vector: pBGSk-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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Zea mays
Bukaryotz, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (bases 1 to 949)
Whitelaw, C. A., Ouckenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                                 EcoRI; 0.6-1.0 kb high
  241 AAAAAAACAGCCCATTAAGGGACCATTAGAATGCGCGCTGCTCCA-TTTTTTTATATAT
                                                                               300 AGAGATATGAGTTGTTGCTCACTAGGCCACTCCACCTCGCATGCGTGTTTTTTATTACAT
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Pred. No. 1e-70;
0; Mismatches 76; Indels 3;
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/strain="By3"
/db xref="t-axon:4577"
/clone="ZMMBTa0748C09"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site_1: Bc
CoT selected genomic DNA library"
                                                                                                                                                                                GAAAAATGAGCCGCTGCTTTTGCATTAAGGGCCTAGAGAT
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1. .949
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Unpublished (2003)
Other_GSSs: PUFWI17TD
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CG041829
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ilarity 84.5%;
Conservative 0
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Class: sheared ends.
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Best Local Similarity
Matches 432; Conserv
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985 bp DNA linear GSS 21-AUG-2003 PUFYZ51TD ZM 0.6 1.0 KB Zea mays genomic clone ZMWBTa0765106, G17503 SEQUENCE.
                                                                                                                                                               965 GTGTTAAGAACCCCTTGTTACCGAGTGTAGTCCAA-GGCTGCTTAACTGAATAATAGTAG 1023
                                                                                                                                                                                                                                           1024 AACACAAGGAGACAAGAGTGTAGAGGAACTGATTCTTTGTTACTATATGGTGCTGCTC 1083
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Dases 1 to 985)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                516 TCCAAGGGTTACATGATATGAGGATCTCCTCTATTTATAGACAAAACTAGGATTTCAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          982 Arcarccacricaaraaaarcricricararcracarcracarccaccricricriciciosciarir 923
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                                 847 GCTTTTCATGTATGTGCTTGAATAGAGGAAAGAATAATATTACAT--AAAATATGAGT
                                                                                                                                                                                                  636 GIGITAAGAACCCCTIGCTACCGAATGTAGTCCAAGGGCTGCTTAACTGAATAATAGTAG
                                                                                                                                                                                                                                                                                 576 AACACAAGAAGACAAGAGTGTAGAGAGGAACTGATTCTTTGTTACTATATGGTGCTGCTC
                                                                                                                                                                                                                                                                                                                      1084 TCCAAAGGTTACATGATATGGGGATCTCCTCTTTATTATAGACAAAACTAGGGTTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-888-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
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/clone="xxmBTa0765106"
/clone lib="xxm 0.61.0 KB"
/note="Vector: pCR4-TOPO, Site 1:
CoT selected genomic DNA library"
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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Other GSSs: PUFYZ51TB
Contact: Cathy Whitelaw
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TIGCAATICGICCGCGICGGIGCACACGICCCTGGICCGGCTIGCCGGCITIGCCCTGGC 1467
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(bases 1 to 879)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Besnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                   301 GTAGTCCCTGTGTACGTCCTAGCAACGATCCGCACCGAGCTCGCCAGTTTTGCTCGTTAGT 360
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                  876 TAAAATAAACGTGTGCATCATATGTGATTGATCGACGTGTGTCAGCGACTTTAAGTCAGC
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                                                                            CTCGCGCGCGACGTGCCCGCGTCTCCCCACGGACGGCTATAAAAAGGCGGCCCACCTGA
                                                                                                                 181 CTCGCGCGCGCGCGCGCGCCCCCCCCCGGGCGCCTATAAAAGGCGGCGCCCCCGA
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Pred. No. 1.1e-69;
0; Mismatches 52; Indels
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/clone=lib="ZM c 6 1.0 KB"
/note="Vector: pCR4-TOP0, Site_1:
CoT selected genomic DNA library"
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/strain="B73"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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Unpublished (2003)
Other_GSSs: PUFVU43TD
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CG118361
CG118361.1 GI:34001798
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88.2%;
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Best Local (
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CG118361/c
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1057 ATTCTTTGTTACTATATGGTGCTGCTCTCCAAAGGTTACATGATATGGGGATCTCCTCTC 1116
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The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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Zea mays subsp. mays
Eukaryotas subsp. mays
Eukaryotas viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Calde; Panticoideae; Andropogoneae; Zea.

(Dases 1 to 993)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
                                                                                                                                               819
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                                                                                                                                                                                                                                                                                                                880 GAATAATATTACAT--AAAATATGAGTTCAACATCTTTCTTAATACCTTTTGCTCGATCT 937
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                                                                                                      449 GIIGIGIIGICCITITIGGIIATAIAIAAAIAAACGIGIGCAICATAIGIGAITGAIC
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                     Indels
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190 Frelinghuysen Road, Piscataway, NJ 08854,
Tel: 732 445 3801
Fax: 732 445 5735
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  Pred. No. 2.1e-60;
0; Mismatches 66
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/cultivar="B73"
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/db_xref="taxon:4578"
/clone="ZMMBBc0349F01"
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Location/Qualifiers
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  84.6%;
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Best Local Similarity 84.6
Matches 380; Conservative
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Class: BAC ends
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 776)
Nhitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                           CAAATCAGCAACAATCACGTGTGCATCCCCATCGACTTCGTGAGCAATAAATCTACTC 863
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                                                                                                                           862 GGGGATTTGTGCTTTTCATGTATGTGCTTGAATAGAGAAAAGAACAATATTACGCATA
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      CAAATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTGGGGGATAAATCTGCT-
                                                                                                                                                                       AAATATGAGTTCAACATCTTTCTTAATACCTTTTTGCTCGATCTCCTTAGTAGAGCCACGT
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/clone="xxMBTa666c01"
/clone lib="xxM 0.6 1.0 KB"
/note="Vector: pCR4-TOP0; Site 1:
Cor selected genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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CG113123
CG113123.1 GI:33996560
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Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J.
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                                     Maize Genomics Consortium
Unpublished (2003)
                                                                   Other GSSs: PUFUD53TD
Contact: Cathy Whitelaw
                                                                                                                                                                          Seg primer: TR
Class: sheared ends.
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                          Bennetzen, J.
         Resnick, A.,
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Matches 343
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a; Poales; Poaceae; PACCAD
              /clone_lib="ZMMBBc"
/note="Vector: pTARBAC1.3; Site_1: BamH1; Site_2: BamH1"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 844)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
                                                                                                           38;
                                                                              993;
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                                                                         Score 262.8; DB 29; Length
Pred. No. 3.7e-48;
0; Mismatches 142; Indels
 coli DH10B"
/lab_host="E.
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Best Local Similarity 73.4%;
Matches 496; Conservative
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 TIGGGGACTICAIGTCAGCAACACTCACGTGTTCATTCTATCGACTTCGAGTCGGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       768 TCGGCGATITCAAATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 TGAATAGAGTCTCATGC-TGATAACGTGTTAAGAACCCCTTGCTACCGAGTGTAGTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTGTTACTATATGGTGCTGCTCTCCAAAGGTTACATGATATGGGGGATCTCCTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                         ECORI; 0.6-1.0 kb
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CG124360
CG124360.1 GI:34007797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 250.4; DB 29; Length 844; llarity 77.8%; Pred. No. 2.2e-45; Conservative 0; Mismatches 88; Indels 10;
            USA
         20850,
                                                                                                                                                                                                                                                                                 /clone lib="ZMMBTa0733310"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOP0; Site_1:
COT selected genomic DNA library"
         ₽
9712 Medical Center Drive, Rockville,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                            organism="Zea mays"
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1059 TCTTTGTTACTATATGGTGCTGCTCTCCCAAAGGTTACATGATATGGGGATCTCCTCTTA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000 -GGCTGCTTAACTGAATAGTAGAACACAAGAGACAAAGAGTGTAGAGAAGAACTGAT 1058
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 AAATCTGCTAGGGATTTGTGCTTTTCATGTATGTGCTTGAATAGAGAGGAAAGAATAA-- 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 ITAGIAGAGCCACGIGCGIGATAACGIGITAAGAACCCCTIGITACCGAGIGTAGICCAA 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 TGAATAGAGTCTCATGC-TGATAACGTGTTAAGAACCCCTTGCTACCGAGTGTAGTGCCAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 ATAATCAGCTAAGAAATGATCATATATGTAATATGAAAAAGGAAAAACAGGATTCAAAAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              886 -----TATTACATAAAATATGAGTTCAACATCTTTCTTAATACCTTTTGCTCGATCTCC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      768 TCGGCGATTTCAAATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGCCGAT 827
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 914)
Mitclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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/note="Weetor: pCR4_TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 GGGCTGCTTAACTGAATAATAGAACACACAAGAAGACAAAGAGACAAGAGTGTAGAGAAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8%; Pred. No. 2.4e-45;
Matches 343; Conservative 0; Mismatches 88; Indels 10;
                                                                                                                                                                                                                            TICK
9712 Medical Center Drive, Rockville, MD 20850, USA
712 Medical Center Drive, Rockville, MD 20850, USA
712 Medical Center Drive, Rockville, MD 20850, USA
713 101-838-5803
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 914
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                                                                                                                                            Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUJFD11TD
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
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Search completed: September 2, 2004, 10:43:41 Job time : 3932 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	September 2, 2004, 12:09:10 ; Search time 19145 Seconds (without alignments) 3753.604 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-732-721-1 1658 1 gaattcacggctcacaatacctcgttagtttgggacggcg 1658
Scoring table:	OLIGO NUC Gapop 60.0 , Gapext 60.0
Searched:	3470272 seqs, 21671516995 residues
Word size :	0
otal number of	Total number of hits satisfying chosen parameters: 6940544

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

em\_ro: \*
em\_sts:\*
em\_un:\*
em\_ui:\*
em\_ui:\*
em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_mus:\*
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gb\_ni:\*
gb\_ow:\*
gb\_ov:\*
gb\_pt:\*
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em\_om:
em\_or:
em\_ov:
em\_ov:
em\_pat:
em\_ph: GenEmbl:\* Database :

Pred. No. is the number of results predicted by chance to have a em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

em\_htg\_vrt:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	6	Query				
	SCOLE	Match	Length	DB	ID	Description
-	25	i T	iù		AC125659	
N	25			1 0	374	27423 Rattu
	23	٦.	-	σ	091	3127 Home
Ω 4	23	1.4	174933	σ	AC009087	9087
	23		ã	7	22	5277 Ratt
	22		592	4	AY285636	36 Sus
	22			9	8	883 Segn
	22			~	99	5677 Oryza
	22			~	87	15
10	22			Ŋ	161	5118 Mus mu
1	22			20	AC122370	Mug
-	22			10	AL596446	AL596446 Mouse
c 13	22			7	AC136065	Ŋ
14	22			N	AC117089	AC117089 Rattus
c 15	22			~	AC099439	6
16	22			~	AC120700	700 Rattus
-	22			N	AC098167	67 Rattus
٦	22			~	AC125267	267 Mus mus
c 19	22			~	AC093979	79 Rattilg
N	22			7	AC122960	960 Rattus
21	22			7	AC124647	547 Mus mus
c 22	22	1.3	290002	7	AC134106	6 Rattus
23	22			7	AC110321	1 Rattue
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300	77		11915	٦,	AE009922	AE009922 Pyrobac
31	77		28573	m	AF024502	
32	21	•	31219	N	AC019857	AC019857 Drosophil
m	21	•	39000	σ	AP003024	
c 34	21	•	69646	~	AC102089	89 Mus m
35	21	•	73746	N	AC101286	Mus
36	21	•	93216	9	AC003016	Huma
37	21	•	98535	6	AF188025	Homo
38	21	•	99150	σ	962	HOHO
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AC125659 262181 bp DNA linear HTG 13-NOV-2002 Rattus norvegicus clone CH230-11B1, WORKING DRAFT SEQUENCE. AC125659 RESULT 1
AC125659
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SCYWCRDS
SOURCE
ORGANISM

REFERENCE AUTHORS

ACLISESS.3 GI:24940742
HTG: HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.
HTG: HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.
HTG: HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 262181)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,

table.

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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranake, D., Barnsteadd, M., Benalmed, F., Biswalo, K., Blatk, C., Blankenburg, K., Blyth, P., Brown, M., Bankenburg, K., Blyth, P., Brown, M., Calderon, E., Cardens, V., Carter, C., Cassar, H., Calderon, E., Cardens, V., Carter, K., Cavasca, E., Cardens, V., Carter, K., Cavasca, E., Cank, C., Cock, C., Cock, C., Cock, C., Cock, C., Cock, C., Cock, C., Cock, C., Cock, C., Ding, Y., Cank, C., Dederich, D., Denson, S., Derawo, C., Ding, Y., Palls, T., Fan, S., Falls, M., Degan, R., Becotto, M., Bugane, C., Bunn, A., Durbin, K., Dural, B., Saves, K., Braser, C., Carser, C., Palls, T., Fan, S., K., Draper, H., Dugan, Rocha, S., Enlly, M., Falls, M., Gartz, M., Gebregeorgis, B., Gaer, K., Gartz, M., Gartz, M., Gebregeorgis, B., Gaer, K., Hadgy, N., Potbes, L., Poster, M., Gebregeorgis, B., Gaer, K., Hadgy, N., Potbes, L., Maniton, K., Hanlton, K., Hanlton, K., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, M., Hanli, C., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, M., Hanli, C., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, C., Hanlton, C., Manlton, M., Hanli, C., Hanlton, C., Hanlton, C., Maniton, M., Hanli, C., Hanlton, C., Maniton, C., Kath, C., Lebow, H., London, P., London, P., London, P., London, P., London, C., Maniton, C., Maniton, M., Malloy, M., Malloy, C., Kath, C., L., Lebow, H., London, P., London, C., Maniton, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M., 
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Submisted (29-JUN-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Bylor plaza, Houston, TX 77030, USA

1 Chases 1 to 262181)

Rat Genome Sequencing Consortium.

Direct Submission

Submisted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:22772668.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and wholes.

The feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs are ordered and oriented, and separated by sized gaps within a contigs caffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
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JOURNAL
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TITLE
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JOURNAL
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REFERENCE

JOURNAL

REFERENCE AUTHORS

COMMENT

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Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS
***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny, D. Marie., Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Baca, E., Baden, H., Anyalebechi, V., Anyagi, A., Aydelji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blath, P., Berown, M., Bryant, N., Bubrch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                    is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 25; DB 2; Length 262181;
100.0%; Pred. No. 0.17;
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ....
                                                        Web site: http://www.hgsc.bcm.t
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242133 credecedadadadarricritadea 242157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1167 CTGGCCCAAGAAAGGTTTCTTAACA 1191
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                                                                                                                       Center project name: GDVZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CH230-11B1"
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/note="wgs_contig"
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261087, .262181
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                                       Center code: BCM
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clavez, D., Clevell, R., Cox, C., Coyle, M., Cree, A., D'Soura, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, Davila, M. Davis, C., Dray, M., Draper, K., Duval, B., Baves, K., Bagan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farner, T., Carza, M., Gabris, A., Ganta, R., Garta, R., Malla, R., Mallo, R., Mallo, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin
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The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, py sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Consensus quality: 204050 bases at least Q40
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Rat Genome Sequencing Consortium.
Direct Submission
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TITLE

COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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Consensus quality: 209444 bases at least Q30 Consensus quality: 212955 bases at least Q30 Estimated insert size: 204859; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 16 clone RP11-498D10, complete sequence.
AC009127
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100.0%; Pred. No. 0.17;
.ive 0; Mismatches 0; Indels 0;
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12448: gap of unknown length
251860: contig of 239412 bp in length
255729: contig of 239412 bp in length
255729: contig of 3769 bp in length
255829: gap of unknown length
268931: contig of 13102 bp in length
268931: gap of unknown length
270715: contig of 1864 bp in length
270815: gap of unknown length
274240: contig of 3425 bp in length
274340: gap of unknown length
274340: contig of 23425 bp in length
274340: gap of unknown length
277282: contig of 2942 bp in length
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2 (bases 1 to 173222)
DOE Joint Genome Institute.
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/db_xref="taxon:10116"
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37204. .99317
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WI-15979 G21275
WI-10173 G11750
WI-17126 G21504
WI-9359 G06054.
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                                                                                           Direct Submission

Submitted (12-APR-2002) Production Sequencing Facility, DOE Joint Submitted (12-APR-2002) Production Sequencing Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 12, 2002 this sequence version replaced gi:13786311.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 Mp.

Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN 1 file.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 173222)

DOE Joint Genome Institute.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174933)
Dis Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                         This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero.
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v 100.0%; Pred. No. ...
0; Mismatches
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/clone="RP11-498D10"
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DOE Joint Genome Institute.
Direct Submission
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Best Local Similarity 100.0
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Nature., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Angulano, D., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Angulano, D., Anglebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Angalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balankenburg, E., Blyth, P., Erown, M., Balankenburg, K., Blyth, P., Brown, M., Brant, D., Burch, D., Burrell, K., Calderon, E., Cardens, V., Carter, K., Cavezos, I., Casar, H., Center, A., Chacko, J., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L. Davisla, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D. Delgado, O., Denson, S., Deramo, C., Ding, Y., Dival, B., Davy, K., Dugan-Rocha, S., Durnha, K., Durbin, R., Davya, K., Draper, H., Dugan-Rocha, S., Durnha, Y., Durbin, R., Davya, K., Egan, A., Escotto, M., Eugene, C., Brans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Garza, M., Gabsia, A., Handis, S., Hume, J., Idhebird, D., Jackson, A., Hannadez, R., Hines, S., Hanes, R., Henderson, N., Hernandez, T., Garza, M., Henlins, B., Howells, S., Hume, J., Idhebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, M., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, 
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-, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
wullty: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 1.
STS Content:
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC115277 184391 bp DN
Rattus norvegicus clone CH230-372C1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .174933
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Alexander, L.J., Morrison, L.Y. and Farenkrug, S.
Direct Submission
Submitted (29-APR-2003) Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave, St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.4%; Score 23; DB 2; Length 184391; Best Local Similarity 100.0%; Pred. No. 2.1; Matches 23; Conservative 0; Mismatches 0; Indels 0;
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  184391: contig of 184391 bp in length.
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100.0%; Pred. No. 8.5;
tive 0; Mismatches 0; Indels
                                                                               organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                         /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                 /note="wgs end extension
clone end:Sp6"
1705._.3257
                                                                                                      /mol_type="genomic DNA"
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/clone="CH230-372C1"
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/db_xref="taxon:9823"
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/note="wgs_contig"
complement [182070. .182
/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence:BZ216963"
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/organism="Sus scrofa"
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/note="microsatellite"
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/note="clone_boundary
clone_end:Sp6
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                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:T7
                                                        . .184391
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These 22; Conservative
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AUTHORS
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194609.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence ontigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
           Nanckelemeh, O., Newlow, N., Ngyren, N., Nortisb. S., Nordselemeh, O., Okudomu, G., Olarnpunsagoon, A., Pall.S., Parks, K., Pasternak, S., Paul, H., Perez, A., Pepevic, D., Primus, B., Pul.L. L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pul.L. L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scotl, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walght, D., Wright, R., Wull, Yakub, S., Yen, J., Yakub, S., Yen, J., Yoon, V., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weight, D., Wright, R., Weiss, R., Thow, J., Yakub, S., Yen, J., Yoon, V., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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COMMENT

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MAM 30-JUN-2003

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Gaps

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Gaps

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ACCESSION VERSION

AX653883/c

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

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E 2 (Dases I to 150876)
S Hahn,J.-H. and Kim, H.-I.
Direct Submission
Direct Submission
Submitted (31-37N-2002) Rice Genome Sequencing Project, National
Institute of Agricultural Science and Technology (NIAST), RDA, 249
Secdun-dong, Suwon 441-707, Korea (E-mail:jhhahn@rda.go.kr,
Tel:82-31-290-0309, Pax:82-31-290-0308)
* NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG 31-JAN-2002
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Ehrhartoideae, Oryzeae, Oryza,
Ehrhartoideae, Oryzeae, Oryza,
I (bases 1 to 150876)
Lee,J.-S., Hahn,J.-H., Yoon,U.-H., Yun,D.-W., Lee,M.-C., Eun,M.Y.
and Kam,H.-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group) chromosome 9 clone
OSJNBa0087J09, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/mol type="qenomic DNA"
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7.5;
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                                                                                                                                                                                                            Score 22;
Pred. No.
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                                                                          /db xref="taxon:39947"
/chromosome="9"
/clone="0J1011_C06"
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/clone="OSJNBa0087J09"
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/variety="Nipponbare"
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100.0%; Pre
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HTG; HTGS_PHASE1.
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Local 22; Conservative
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AC108761/c
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NoTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                               , Hou, Y.M., and Zou, G.
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                                  PAT 22-MAR-2003
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Direct Submission
Submitted (05-SEP-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC clone:OJ1011 C06
Published Only in Database (2002)
2 (Bases 1 to 109964)
                                                                                                                                                                                                                                                                                                          Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. a Plant genes involved in defense against pathogens Patent: WO 03000898-A 3753 03-JAN-2003;
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8.2;
                                  linear
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Oryza satīva (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta,
                               AX653883 2409 bp DNA Sequence 3753 from Patent W003000898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 22; DB 100.0%; Pred. No. 8.2 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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HTG; HTGS_PHASE2.
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Matches 22; Conservative
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                                                                                                                                                                                       Oryza sativa
                                                                                                                                                             Oryza sativa
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

JOURNAL

AUTHORS TITLE

REFERENCE

AP005677/c LOCUS

RESULT 8

source

FEATURES

Query Match

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ORIGIN

source

FEATURES

JOURNAL

TITLE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 17645)
Berghoff, A., Haakenson, W., Bielicki, L. and Meyer, R.
The sequence of Mus musculus BAC clone RP23-45988
                              Center for Genome
                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC122370 176045 bp DNA linear ROD 11-NO<sup>*</sup>
Mus musculus BAC clone RP23-459B8 from chromosome 8, complete
                    Submitted (15-DEC-2003) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 15, 2003 this sequence version replaced gi:28460918.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
-------- Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64657: contig of 9810 bp in length
64757: gap of 100 bp
101040: contig of 36283 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13387: contig of 13387 bp in length
13487: gap of 100 bp
18518: contig of 5031 bp in length
18618: gap of 100 bp
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gap of 100 bp
contig of 13604 bp in length
gap of 100 bp
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151468: contig of 21174 bp in length.
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Web site: http://www-seq.wi.mit.edu
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100.0%; Pred. No. 7.4;
iive 0; Mismatches
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/organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                         Center project name: 123300
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Lister Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 151468)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Bodguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., Exickson, J., Farreixe, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Ferreixe, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Indblad-Toh, K., Kartas, A., Kells, C., Landers, T., Levine, R.,

Indblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

O'Neil, D., Oliver, J., Peterson, K., Petta, R., Rise, C., Rogov, P., Roman, A., Stange-Thomann, V., Schuben, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, V. S., Viel, K., Travers, M.,

Vassiliev, H., Verkataraman, V. S., Viel, K., Zimmer, A. and Zody, M.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                 Gaps
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0
             1.3%; Score 22; DB 2; Length 150876; 100.0%; Pred. No. 7.4; tive 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                             AC116118 151468 bp DNA linear
Mus musculus chromosome 16 clone RP23-73P19 map 16,
IN PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS PHASE1; HTGS FULLTOP; HTGS ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 16, clone RP23-73P19
                                                                                                                                             118775 cGACGACGTCGACGCTGATGCT 118754
                                                                                                   657 CGACGACGTCGACGCTGATGCT 678
                                                                                                                                                                                                                                                                                                                                                     AC116118.5 GI:39841503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 151468)
Query Match
Best Local Similarity 100.0
Marches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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AUTHORS
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KEYWORDS

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ROD 11-NOV-2003

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TITLE JOURNAL

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AUTHORS

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TITLE JOURNAL

COMMENT

JOURNAL

REFERENCE

JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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1365. .4836
rpt_family="MER2_type"
124. .7496
clone_lib="RPCI-23"
...165
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8969_ .9414
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1900. .12045
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Submitted (11-NOV-2003) Department of Genetics, Washington
Submitted (11-NOV-2003) Department of Genetics, Mashington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 14, 2003 this sequence version replaced gi:28016323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                             Submitted Country 2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (Dases I to 176045)
McPherson, J.D. and Waterston, R.H.
Direct Submitted (29-JAN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (Dases I to 176045)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this schone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-PEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 176045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/67 mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC117189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: M BA0459B08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                        3 (bases 1 to 176045)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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                                                                Sequencing of Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WUGSC
                         2 (bases 1 to 176045)
Wilson,R.
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      Jnpublished (2001)
                                                                                        Unpublished (2001)
                                                                                                                                                Direct Submission
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clone="RP23-459B8"

FEATURES

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1. .191735
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                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-386E10"
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 100.
Matches 22; Conservative
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HTG; HTGS PHASE1
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AC136065/c
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VERSION
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                                                                                                                                                                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracey, A.

Direct Submission

Submitted (Ve. APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:17043843.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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17668. .37812
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41599. 41601
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31663. .33668
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33667. .33893
                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="B4"
8203. .38420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                 family="L1"
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                                .31287
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9026. .39165
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                 /rpt_fa
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; IT:, TREMBL; WD:, WORMPEP; Information on the WORMPEP HTT. (Nums sance on the found att.)
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Rattus.

Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benamed, F.,
Baldwin, D., Bandaranaike, D., Burber, M., Barnstead, M., Benamed, F.,
Bayant, M., Burdh, P., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavacos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Toyle, M., Cree, A., Din, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Ganta, R., Ganta, A., Gante, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-386E10 is
from the RPCI-23 Mouse PAC Library—
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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gap of unknown length
contig of 2553 bp in length
gap of unknown length
contig of 1521 bp in length
gap of unknown length
contig of 1961 bp in length
gap of unknown length
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g of 3362 bp in length
f unknown length
g of 1789 bp in length
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contig of 1813 bp in length
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, Y., Liu, W., Loudon, P., Longacre, S., Lopez, J., Louseged, H., Lozado, R.J., Liu, X., Mandu, M., Malloy, R., Martinez, B., Mapua, P., Martin, R., Martinez, R., Martinez, B., Mapua, P., Martin, R., Martinez, R., Martinez, B., Mapua, P., Martin, R., Martinez, R., Milosavjevic, A., Minero, S., Moleod, M., Montell, T., Meenen, E., Milosavjevic, A., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Ngyren, N., Norris, S., Naschemen, E., Milosavjevic, A., Nerzi, M., Nair, L., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Reyier, M.A., Reigh, R., Reilly, B., Reilly, M., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Rose, M., Rose, K., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Strong, K., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Wang, S., Warren, J., Waldron, L., Walker, B., Wang, J., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, S., Wang, C., Wang, C., Wang, S., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R., Wang, C., Wang, R
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 146097 bases at least Q40
Consensus quality: 151106 bases at least Q30
Consensus quality: 155140 bases at least Q20
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gap of unknown length
contig of 1510 bp in length
gap of unknown length
contig of 1221 bp in length
gap of unknown length
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gap of unknown length
contig of 1398 bp in length
gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
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Center: Baylor College of Medicine
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Center clone name: CH230-85M19
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Rat Genome Sequencing Consortium.
Direct Submission
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Rayalebechi, V., Aoyagia, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Baca, E., Baden, H., Anyalebechi, V., Aoyagia, A., Ayadeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bandaronaike, D., Burrell, K., Calderon, E., Carderon, C., Carter, K., Carter, K., Carderon, E., Carter, K., Carter, K., Carderon, C., Chan, Y., Chan, Y., Chen, Z., Chu, J., Clackoo, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Darmo, C., Ding, Y., Dinh, H., Divya, K., Eraper, H., Duyan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., R., Fall, G., Fernandez, S., Finley, M., Paggo, N., Carcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, K., Garcia, A., Garner, T., Garza, M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Haaland, W., Haaland, W., Hamilton, C., Hamilton, K., Havlak, P., Hawes, A., Hangen, B., Howells, S., Hladun, S.L., Hodgson, A., Hodles, M., Hines, S., Hladun, S.L., Hodgson, A., House, J., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensule, D., Mahned, M., Malloy, K., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Mahner, E., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Mangum, B., Mapula, P., Martin, R., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, E., Martine, M., Mangum, M., Martine, E., Martine, E., Martine, E., Martine, E., Martine, M., Martine, M., Martine, M., Martine, M., Martine, M., Martine, M., Martine, M., Martine,
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Rattus norvegicus clone CH230-119G9, WORKING DRAFT SEQUENCE, 2
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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egap of unknown length
contig of 3113 bp in length
gap of unknown length
contig of 3845 bp in length
gap of unknown length
contig of 4392 bp in length
gap of unknown length
contig of 4269 bp in length
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gap of unknown length
contig of 3544 bp in length
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Matches 22; (
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KEYWORDS
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SOURCE

LOCUS

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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 15, 2002 this sequence version replaced gi:23194925. The sequence in this sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Norgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Narris, S., Nankervis, C., Neal, D., Newton, N., Ngryen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Paaco, M., Quiroz, J., Rachlin, E., Reves, K., Regier, M., L.-Er, Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, M., Riggs, F., Sanders, W., Savery, G., Scherr, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Schartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sheity, J., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Warish, M., Strong, R., Waldron, L., Walker, B., Wang, J., Wallson, R., Wallson, R., Walson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yan, J., Yoon, L., Yoon, V., Willsams, G., Wallson, R., Walson, R., Walson, R., Weiss, R., Weiss, R., Weiss, Smith, D., Norley, K., Weiss, Smith, D., Norley, R., Mann, S., Smith, D.R., Holt, R., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA

3 (Dases 1 to 197981)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 197981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a "working draft' sequence It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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Worley, K.C.
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1 (Dasses I to 215867)

Anyalabechi, V., Anyagia, A., Ayodeii, M., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Anyagia, A., Ayodeii, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bradencas, V., Carter, K., Carch, P., Surchl, R., Calderon, E., Chardro, J., Chaver, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Darson, S., Deramo, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Darson, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Carner, T., Garza, M., Carber, H., Carser, C.M., Gabisi, A., Garris, M., Falag, N., Fortbes, L., Foster, M., Gabisi, A., Garris, R., Garcia, R., Garris, M., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gabregoorgis, E., Geer, K., Gill, R., Garcia, A., Garra, M., Gebregoorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Harnardez, S., Haland, W., Hanil, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Handerson, N., Hernandez, M., Hoolels, M., Haldin, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hung, L., Johnson, R., Johnson, R., Johnson, R., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, S., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, Mahmud, M., Maltin, K., Mattin, R., Mahmud, M., Martin, K., Mattin, R., Mander, S., Mulecd, M. P., Mattin, K., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Mattin, R., Pala, S., Paul, M., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R., Pala, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC099439 215867 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-145P16, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 22; DB 2; Length 197981;
100.0%; Pred. No. 7.4;
                      1 196422: contig of 196422 bp in length
196423 196522: gap of unknown length
196523 197981: contig of 1459 bp in length.
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                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                end sequence:BH315129"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 22; Conservative

    be preserved.

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AC099439/c
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VERSION
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PRINCES OF CONTROL NOTING AND SEAD IN E. Resease X. Register M. Siggis P. S. Hitself, S. Redity, B. Relling, M. Rennin, S. Resease, X. Resear, S. R. Piggis P. S. Hitself, S. Rodky, T. Kojsa, M. Nose, M. Nose, R. Rinki, S. Bratty, S. Sheri, S. She
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/note="wgs_contig"
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Title: Perfect score:

1 gaattcacggctcacaatac......tccgttagtttgggacggcg 1658 Sequence:

US-10-732-721-1 1658

, Gapext 60.0 OLIGO NUC Gapop 60.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

0 Word size :

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

N Geneseq\_29Jan04:\* 1: geneseqn1980s:\* 2: geneseqn1990s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2000s:\* geneseqn2002s:\* . 99: 10: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

## SUMMARIES

	Description	Ada70430 Rice gene	Aac50800 Arabidops	Aac33054 Arabidops	Abk31369 Signal tr	Abl70326 Chemicall	Aas61273 Human gen					Ada49079 Wheat gen	Acc61661 Gene sequ	Aaz52423 HTRM clon		Human	Adb48928 Novel hum		Aai99684 Human TNF	Abk28382 DNA trans	Aak80680 Human imm	Abz74054 Secreted	Adc20775 Human sec	Aai62620 Human bre
	di i	ADA70430	AAC50800	AAC33054	ABK31369	ABL70326	AAS61273	ABL07848	ABL07850	ABN17338	AAL15883	ADA49079	ACC61661	AAZ52423	AA160732	AAI58946	ADB48928	ADA53534	AAI99684	ABK28382	AAK80680	ABZ74054	ADC20775	AAI62620
	B	1	m	c	9	9	9	4	4	9	4	8	7	m	4	4	8	7	4	9	4	7	σ	4
	Length DB	2409	801	802	5956	5956	5956	16739	21828	291	785	830	1044	1963	1973	1979	1979	3255	4633	5823	12988	12988	12988	16163
* Ouerv	Match	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2
	Score	22	21	21	21	21	21	21	21	20	20	20	20	20		20	20	20	20	20	20	20	20	20
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AAK83901 AAK87161	AAL03817	ABQ88176	AAF08066	ABN87803	ABZ54983	ABK85714	AAK59627	ABK99945	AAK75762	AAV08179	AAV68162	AAN30041	ABS53995	AAN30039	AAV08177	AAV68160	ABS53993	ADD30329	ABZ31860	ABQ67825
16163 4 16163 4	16163 4	301 6	558 3	604 6	648 7	734 6	771 4	9116	087 4	1447 2	1447 2	1449 1	1449 6	1469 1	1469 2	1469 2	1469 6	1484 9	1551 6	557 6
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24 25	c 26	27	c 28	c 29	G 30	31	c 32	C 33	c 34	c 35	c 36	c 37	c 38	c 39	۵ 40	c 41	c 42	c 43	C 44	c 45

## ALIGNMENTS

BP. ADA70430/c ID ADA70430 standard; DNA; 2409 (first entry) Rice gene, SEQ ID 3753. 20-NOV-2003 ADA70430; RESULT 1 

Plant, bacterial infection, fungal infection, viral infection, rice, gene, ds. dene;

Oryza sativa.

WO2003000898-A1.

03-JAN-2003.

22-JUN-2001; 2001WO-IB001105.

22-JUN-2001; 2001WO-IB001105.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Goff SA, Hou Y; s Z, Zhu T, Zou G; Glazebrook J, Goff Whitham S, Xie Z, Cooper B, S, Tao Y, Chang H, Chen W, Co Katagiri F, Quan S,

WPI; 2003-175290/17.

t t Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression

Claim 6; SEQ ID NO 3753; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to

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9905-0144065P

9905-0144331P

9905-0144331P

9905-0144332P

9905-0144332P

9905-0144334P

9905-0144335P

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9905-0146638P

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 illustrate the invention.
                                                                                                                                                                                                                                      Arabidopsis thaliana
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pathway;
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XW Promoter; termination

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XX Arabidopsis py005-0

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XX Arabidopsis py005-0

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Cell signalling, cytosine methylation, cell signalling disease, cancer, tumour; cytostatic; ds.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2002-154758/20

(EPIG-) EPIGENOMICS AG.

29-JUN-2001; 2001WO-EP007471. 30-JUN-2000; 2000DE-01032529 01-SEP-2000; 2000DE-01043826

VO200202807-A2

10-JAN-2002.

Unidentified

Chemically treated cell signalling DNA sequence complementary to#108.

(first entry)

01-JUL-2002

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signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method of cor the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genemic DNA can be obtained from cells or callular components which contain DNA, e.g. cell innes, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK1158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed succertly from the
                                                                                                                                                                             Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to chemically modified DNA sequences of
                                                                                                                                       Signal transduction associated gene modified complementary DNA #106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5956 BP; 1652 A; 171 C; 1433 G; 2700 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001; 2001WO-EP007472.
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                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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Best Local Similarity
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                                                                                                                                                                                                                                                               Homo sapiens
                                                                                              23-APR-2002
                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                  Synthetic.
                                                      ABK31369;
ABK31369
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligoners for detecting cytosine methylations, as well as a method which is considered by a particularly suitable for the diagnosis and/or therapy of genetic and chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as sociated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as sociated with cell signalling. Note: The sequence data for this patent is not represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammardory response; Haemophila; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 21; DB 6; Length 5956;
100.0%; Pred. No. 11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene regulation-associated gene oligonucleotide #228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 216; 24pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS61273 standard; DNA; 5956 BP.
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Best Local Similarity
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Gaps

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Conservative

ABL70326 standard; DNA; 5956 BP

RESULT 5

ABL70326

ABL70326

axa XXa

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The invention relates to 224 nucleic acid sequences comprising at least

18 bases of a chemically pretreated gene associated with gene regulation

20 selected from 43 known genes (or complementary sequences). The chemical

21 pretreatment converts cytosine bases unmethylated at the 5-position to

22 uracil or another base with hybridisation behaviour dissimilar to

23 cytosine, to enable analysis of cytosine methylations. The DNA sequences,

24 coligomers (or sets/arrays) and method are useful in the diagnosis of

25 diseases (or predisposition to diseases) associated with gene regulation

26 diseases (or predisposition to diseases) associated with gene regulation

27 and in therapy of such diseases, by enabling analysis of the cytosine

28 methylation patterns of such genes, kits are provided. They are

28 especially useful in diagnosis and therapy of e.g. severe combined

28 immunodeficiency disease, cardiac disorders, haemophilia, solid tumours

28 and cannoer, Merner syndrome, asthma, HDR syndrome, sathre-chorzen

29 and cannoer, sand is associated with the human gene regulation-associated

20 present sequence is a sequence included in the sequence data for this

20 specification and is associated with the human gene regulation-associated

20 genes. Note: The sequence data for this patent did not form part of the

21 printed specification, but was obtained in electronic format directly

22 from WIPO at ftp.wipo.int/pub/published_pot_sequence
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
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100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequences from chemically modified genes
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100.0%; Fig.
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07-APR-2000; 2000DB-01019173.
30-JUN-2000; 2000DB-01035529.
01-SEP-2000; 2000DB-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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Matches 21; Conserv
                                                                                                                                                                       WO200177375-A2.
                                                                                                                    Homo sapiens
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Myers EW;

PWD,

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Venter JC,

WPI; 2001-656860/75.

P-PSDB; ABB63745.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY

23-MAR-2001; 2001WO-US009231.

Drosophila melanogaster

WO200171042-A2

27-SEP-2001

Claim 1; SEQ ID NO 18026; 21pp + Sequence Listing; English.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster expressed polynucleotide SEQ ID NO 18032.
                                                                                                                                                                                                  Sequence 16739 BP; 4986 A; 3249 C; 3289 G; 5215 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                   Score 21; DB 4; Length 16739; Pred. No. 11;
                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                               2143 TAAATTAAAATTCTATTCTAT 2163
                                                                                                                                                                                                                                                                                                            209 TAAATTAAAATTCTATTCTAT 229
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100.001
5, Fre
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
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ABL07850
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(see Table 1

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29-MAY-2001; 2001WO-US010836.
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29-AUG-2000; 2000US-0228716P.
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P-PSDB; ABP01586.
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                                                                                                                                                                             interactions.
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Best Local 8
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(referred to as open reading frame. ORFX, where X is 1-11491 (See Table 1) in the specification) ABN15762 to ABN2752 encode the human ORFX in the specification) ABN15762 to ABN2752 encode the human ORFX proteins given in ABN500010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders, haemorrhage, costeoarthritis, neurodegenerative disorders mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytckine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                       present invention describes substantially purified human proteins
Disclosure; SEQ ID NO 3153; 1037pp; English.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21828 BP; 6614 A; 4180 C; 4296 G; 6738 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 21; DB 4; Length 21828;
                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 18032; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                      2001-656860/75.
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                                                P-PSDB; ABB63747
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                        Gaps
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                      0; Indels
                                                                                                                                                                                                                                                                      Human ORFX polynucleotide sequence SEQ ID NO:3153.
100.0%; Pred. No. 11; ative 0; Mismatches
                                                                                   7232 TAAATTAAAATTCTATTCTAT 7252
                                                    209 TAAATTAAAATTCTATTCTAT 229
                                                                                                                                                                       BP.
                                                                                                                                                                   ABN17338 standard; cDNA; 291
                                                                                                                                                                                                                                     (first entry)
                    Conservative
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Gaps

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0; Indels

Score 20; DB 6; Length 291;

red. No. 34; Mismatches

Pred.

1.2., 100.0%; Fit

20; Conservative

Similarity

Query Match Best Local S

Matches

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Sequence 291 BP; 107 A; 41 C; 56 G; 86 T; 0 U; 1 Other;

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Human breast cancer expressed polynucleotide 8340.
                                                                                                                                                                      Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang Y, Steinmann K;
                                       BP.
                                     AAL15883 standard; cDNA; 785
                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000; 2000US-0189167P
24-MAR-2000; 2000US-0192099P
29-MAR-2000; 2000US-0193480P
15-MAY-2000; 2000US-020530B
09-JUN-2000; 2000US-0211315P
                                                                                                                                                                                                                                                                                                              10-JAN-2001; 2001WO-US000798
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0220534P
                                                                                                                                                                                                                                                                                                                                                2000US-0176077P
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu Y,
                                                                                                                                                                                                                                            WO200151628-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2000;
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                14-JAN-2000;
                                                                                                       07-DEC-2001
                                                                                                                                                                                                                                                                          19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lillie J,
                                                                     AAL15883;
                     AAL15883/c
RESULT 10
                                     Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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New peptide useful as a marker for the diagnosis of breast cancer.

Length 830;

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ling frame that encodes a polypeptide associated with disease
istance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant;
                                         The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast calls. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                              Seguence 785 BP; 216 A; 172 C; 184 G; 200 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                          / Match 1.2%; Score 20; DB 4; Length 785; Local Similarity 100.0%; Pred. No. 35; of Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheat gene conferring disease resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S, Cooper B, Goff SP
Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 1149; 299pp; English.
              Claim 1; Page 1509; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                    229 TTTTTCCTTAAGAAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                      709 TTTTTCCTTAAGAAAAAA 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2002; 2002WO-IB002453
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA49079 standard; DNA; 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Katagiri F, Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-184052/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reading frame that resistance, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum.
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                                                                                                                                                                                                                                                                   Query Match
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Sequence 830 BP; 177 A; 221 C; 219 G; 213 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
                                                                                                                                                                                                                                                                             complex; eukaryote; drug target; diagnosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kruse UD, Kuester BD;
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                              0; Indels
Score 20; DB 8;
Pred. No. 35;
0; Mismatches
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Superti-Furga GD;
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                                                           1613 GATCCGCGCCGAGCTCGCCA 1632
                                                                                        564
      100.08; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is available on CD-ROM
                                                                                                                                                               BP.
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                                                                                      GATCCGCGCCGAGCTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grandi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ52423 standard; DNA; 1963
                                                                                                                                                               ACC61661 standard; DNA; 1044
                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2001; 2001EP-00111774
   1.2%;
                                                                                                                                                                                                                                                   Gene sequence #SEQ ID 2104
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                               20; Conservative
                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELL-) CELLZOME AG
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gavin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABR53619
                                                                                                                                                                                                                                                                              Multiprotein
                                                                                                                                                                                                                      20-JUN-2003
                                                                                                                                                                                                                                                                                                                                      EP1258494-A1
                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
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                                                                                                                                                                                            ACC61661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         document
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                                                                                        545
                                 Matches
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                                                                                                                                    RESULT 12
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

Human polynucleotide SEQ ID NO 4721.

(first entry)

22-OCT-2001

AA160732;

AAI60732 standard; cDNA; 1973 BP.

AA160732

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(first entry)

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HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; albS; arteriosclerosis; cirtosis; cancer; leukaemia; diabetes mellitus; ss; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                          HTRM clone 2019742 DNA sequence.
                                                                  Homo sapiens
                                                                             W09957144-A2
                24-FEB-2000
                                                                                        11-NOV-1999
                                                                                                                                               Hillman JL,
Gerstin EH,
     AAZ52423;
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peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaner's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                         leukaemia; ss
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
AMAZALIA-2014, ale immain intainstriptional regulator uniquence are uncleotide sequences. The HTRM protein and nucleotide sequences are useful for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell profilerative disorders such as arteriosclerosis and cirrhosis; cancers including adenocarcinoma and leukaemia; immune disorders such as AIDS, Addison's disease, diabetes of militur, rheumatoid arthritis, multiple sclerosis, systemic lugus erythematosus, and myasthenia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for freating or preventing disorders systemic associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques.

CC polypucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by wodulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression. Antibodies which calesoning disorders associated with the expression of HTRM, particularly and associated with the expression of HTRM, particularly and associated with the expression of HTRM, particularly and an associated with the expression of HTRM, particularly and an associated with the expression of HTRM, particularly and an associated which the expression of HTRM, particularly and an associated with the expression of HTRM, and an associated with the expression of HTRM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides useful for diagnosis, prevention and treatment of cancer and
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Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 20; DB 3; Length 1963; 100.0%; Pred. No. 35; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1963 BP; 488 A; 499 C; 491 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevented by aggressive treatment or preventive measures
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Baughn MR, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 155; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                       98US-0084254P.
98US-0095827P.
98US-0102745P.
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Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-052941/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune disorders
                                                                                                                                                                                                                                                                                                                               04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
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02-OCT-1998;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, Wal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian XB,
Yang Y,
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Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as central nervous system injuries.
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                                                                                         21-JAN-2000; 2000US-00468725.
25-APR-2000; 2000US-0055317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-06620312.
                                                                                                                                                                                                                                                       2000US-00662191.
2000US-00693036.
26-DEC-2000; 2000WO-US034263
                                                                  99US-00471275
2000US-00488725
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es 20; Conserva
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                                                              23-DEC-1999;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, impunosuppressant and eyrostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous such as yestem, such as peripheral nervous injuries, peripheral nervous and coloralised neuropathies and central nervous system diseases, such as lacral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                    nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                  peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hacenses; hacensestric; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, Wa
Zhang J,
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            مصنع 4, wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 1149.
                                                                            as central nervous system injuries.
315 TTAAGAAAAAAACAGCCCA 334
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DB 4; Length 1979; 35;

Query Match 1.2%; Score 20; Best Local Similarity 100.0%; Pred. No.

Sequence 1979 BP; 498 A; 505 C; 485 G; 491 T; 0 U; 0 Other;

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completed: September 2, 2004, 13:35:49
ne: 2019 secs
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1661 TTAAGAAAAAAACAGCCCA 1642
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GENERAL INFORMATION:
NAME/KEY: CDS
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Sequence 2, Appli
Sequence 1300, Ap
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Sequence 14, Appl
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Sequence 3, Appli
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Sequence 79, Appl
Sequence 3, Appli
                                                                                                                             September 2, 2004, 13:02:10 ; Search time 144 Seconds (without alignments) 6389.643 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-489-751-93
US-09-134-001C-1009
US-09-328-352-1253
US-08-712-709-6
US-08-711-444-6
US-09-011-444-6
US-09-016-434-772
US-09-016-434-772
US-08-220-240A-4
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US-08-956-171E-520
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US-09-184-418C-14
US-09-621-976-3318
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US-09-103-840A-2
US-09-103-840A-1
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US-08-781-891-79
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US-08-911-020-2
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                                                                                       - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length DB
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1658
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Perfect score:
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3741, Ap
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100.0%; Pred. No. 3.5;
tive 0; Mismatches 0; Indels
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: PolyPeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
NUMBER: OF SEQ ID NOS: 1105
SOFTWARE: PLE_genes Version 1.0
US-09-252-991A-11412
US-08-465-32A-2883
US-08-465-388-4
US-08-465-388-4
US-09-540-237-717
US-09-552-91A-3731
US-09-252-991A-3731
US-09-252-991A-3785
US-09-252-991A-3785
US-09-105-577-21
US-09-105-577-21
US-08-105-577-21
US-08-105-577-21
US-08-111-556A-1
US-09-252-991A-4932
US-08-458-0238-1
US-08-458-0238-1
US-09-252-991A-11395
US-08-252-991A-11395
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US-09-299-378-3
                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                     US-09-620-312D-838/c
; Sequence 838, Application US/09620312D
; Patent No. 6569662
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Chen, Rui-hong
Chen, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ma, Yunging
Wang, Dunrui
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Best Local Similarity 100.0
....hag 20; Conservative
   APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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US-09-620-312D-838
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NAME/KEY: misc feature
LOCATION: (19501). (21000)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (210001). (22500)
OTHER INFORMATION: n=a or or g or t
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LOCATION: (225001).. (24000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (255001).. (27000)
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NAME/KEY: misc feature
LOCATION: (255001).. (2000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (270001).. (285001)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (270001).. (285001)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (285001).. (300000)
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LOCATION: (33001)..(345000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (34501)..(360000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (13501)..(150000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or g or t
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CTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (420001)..(435000)

CTHER INFORMATION: n=a or c or g or OTHER INFORMATION: n=a or c or g or NAME/KEY: misc_feature
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LOCATION: (300001)..(315000)
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LOCATION: (105001)..(120000)
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NAME/KEY: misc_feature
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STHER INFORMATION: n=a or c or
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                                                                            NAME/KEY: misc feature
LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preveriTITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
                                                   US-01-751-389-3/c

Sequence 3, Application US/09751389

Sequence 3, Application US/09751389

Sequence 3, Application US/09751389

Sequence 3, Application US/09751389

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFRENCE: CLOOLO67

CURRENT APPLICATION NUMBER: US/09/751,389

CURRENT APPLICATION NUMBER: 2001-01-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 786431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1%; Score 19; DB 4; Length 786431; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 19; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (90001)...(105000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or
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NAME/KEY: misc feature

LOCATION: (1)...(766431)

OTHER INFORMATION: n = A,T,C or G
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LOCATION: (45001) .. (60000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (60001) .. (75000)
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or
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LOCATION: (1). (15000)
OTHER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-198-452A-1
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NAME/KEY: misc\_feature
LOCATION: (630001).. (645000)
OTHER INFORMATION: nea or c or g or t
NAME/KEY: misc\_feature
LOCATION: (645001).. (660000) WME/KEY: misc feature COCATION: (61501). (630000) THER INFORMATION: n=a or c or g or t NAME/KEY: misc feature
LOCATION: (735001)...(750000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (750001)...(765000)
OTHER INFORMATION: n=a or c or g or t AAME/KEY: misc feature LOCATION: (720001)..(735000) THER INFORMATION: n=a or c or g or t LOCATION: (810001)..(825000)

THER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t MAME/KEY: misc feature LOCATION: (480001)..(495000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc\_feature
LOCATION: (510001)...(525000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc\_feature
LOCATION: (525001)...(540000) NAME/KEY: misc feature LOCATION: (49501)..(510000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (555001)..(570000) OTHER INFORMATION: n=a or c or g or WAME/KEY: misc feature LOCATION: (585001)..(600000) OTHER INFORMATION: n=a or c or g or CCATION: (52501)..(54000)
THER INFORMATION: n=a or c or g or OCATION: (600001). (615000)
THER INFORMATION: n=a or c or g or or WME/KEY: misc feature LOCATION: (660001)..(675000) THER INFORMATION: n=a or c or g or OCATION: (690001)..(705000)
THER INFORMATION: n=a or c or g or OCATION: (70501)..(720000) THER INFORMATION: n=a or c or g or LOCATION: (795001)..(810000)
OTHER INFORMATION: n=a or c or g or LOCATION: (465001)..(480000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (570001)..(585000) OTHER INFORMATION: n=a or c or g AME/KEY: misc feature ACATION: (67501)..(690000) THER INFORMATION: n=a or c or g LOCATION: (54001)..(555000) THER INFORMATION: n=a or c or g OCATION: (64501)..(660000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature misc\_feature (540001)..(555000) AME/KEY: misc feature OCATION: (600001)..(615000) AME/KEY: misc\_feature OCATION: (705001)..(720000) WAME/KEY: misc\_feature GOCATION: (765001)..(780000) MAME/KEY: misc feature LOCATION: (780001). (795000) NAME/KEY: misc\_feature LOCATION: (825001)..(840000) AME/KEY: misc feature NAME/KEY: misc\_feature

Sequence 4810, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Becon et. al
APPLICANT: Gary Becon et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342 GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to TITLE OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P-NI 3864
CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 1090-12-06
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FastSEQ for Windows Version 4.0 ó ·, Gaps Gaps 0 0; 1.1%; Score 19; DB 4; Length 1230025; 100.0%; Pred. No. 9.5; Length 533; 0; Indels 0; Indels 1.1%; Score 18; DB 4; 100.0%; Pred. No. 37; 100.0%; Pred. M. 100.0%; Prec. retive 0; Mismatches OTHER INFORMATION: n=a or c or g or t LOADINEEX: misc feature LOCATION: (845001)...(855000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (85501)...(870000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (870001)...(865000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (805001)...(900000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (805001)...(900000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (900001)...(915000) 1200765 GAGTGTAGAGAACTGA 1200783 1039 GAGTGTAGAGGAACTGA 1057 Sequence 93, Application US/09669751 Patent No. 6551575 689 CTTTTGTTTTTCT 706 263 CTTTTGTTTTGTTTCT Query Match 1.1 Best Local Similarity 100. Matches 18; Conservative Conservative NAME/KEY: misc\_feature Query Match Best Local Similarity Matches 19, Conserva TYPE: DNA ORGANISM: Drosophila RESULT 5 US-09-489-039A-4810 US-09-669-751-93 US-09-669-751-93 SEQ ID NO 93 LENGTH: 533 ઠે δ qq

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Gaps
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US-09-111-444-6/c
; Sequence 6, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION:
; TITLE OF ENDURISOS:
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
           Sequence 6, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 18; DB 100.0%; Pred. No. 36; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive
Palo Alto
                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN PROTEIN INTEREST OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: 1 ADDRESSEE Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DISKETTE
COMPUTER: DISK COMPATIBLE
COMPUTER: STEM COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
IELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1501 CGGCTATAAAAGGCGGC 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908 CGCCTATAAAAGGCGGC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.1
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                           STREET: 31/2.
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MOLECULE TYPE: cl
IMMEDIATE SOURCE:
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STREET: 317
                                                                                                                                                                                                                                                                                                                          ZIP: 94304
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US-08-712-709-6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-712-709-6
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                              Sequence 100, Application US/09134001C

Ratent No. 6380370

GRERRAL INFORMATION:

GREBRAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: WICLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR APPLICATION NUMBER: US 60/055,779

FRIDR APPLICATION NUMBER: US 60/055,779

FRIDR APPLICATION NUMBER: US 60/055,779

FRIDR APPLICATION NUMBER: US 60/055,779

FRIDR APPLICATION NUMBER: US 60/055,779

FRIDR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1253
LENGTH: 1428
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100.0%; Pred. No. 36;
tive 0; Mismatches 0; Indels
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                                                                                                          DB 4; Length 624; 37;
                                                                                                                                                     Indels
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                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 37;
tive 0; Mismatches
                                                                                                          1.1%; Score 18; DB 100.0%; Pred. No. 37; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1253, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                1378 CGCGTCGCGCCGCACGGG 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AAAAAACAGCCCATTAAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 CAAATATTTTAAATGAAT 120
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                                                                                                                                                                                                                                           394 CGCGTCGCGCCGCACGGC 411
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                      TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.15
Best Local Similarity 100.0
Matches 18; Conservative
                                                   ; ORGANISM: Kleusi
US-09-489-039A-4810
                                                                                                                                                                                                                                                                                                                              US-09-134-001C-1009
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    LENGTH: 624
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                                                                                                              Query Match
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US-09-016-434-772/c

Sequence 772, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION

ITILE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
                                                                                                                                                                                               Score 18; DB 3; Length 2311;
Pred. No. 36;
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFORM:
COMPUTER: DECOMPATIBLE
CORRALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: HEREWITH
                                                                                                                                                                                  1.1%; SCC...
100.0%; Pred. No. 30,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPRONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 772:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
                                                                                                                                                                                                                                                                               1501 CGGCTATAAAAGGCGGC 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1501 CGGCTATAAAAAGGCGGC 1518
                                                                                                                                                                                                                                                                                                                     908 cecraraaaaeceec 891
                                                                                                                                                                                             Query Match 1.1
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: MMLRZDT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: sing
                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 18; Conserva
                                                                                                           LIBRARY:
CLONE: Consensus
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CLONE: 477245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-016-434-772
                                                                                                                                                    US-09-541-228-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                              PF-0118 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASUSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0118 US
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTOREEV/ASHIT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0118
TELECOMMUNICATION INFORMATION:
TELEPRAX: 415-855-0555
TELEPRAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908 CGCTATAAAAAGGCGGC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2311 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIANY:
LIBRARY:
TONE: Consensus
                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 For
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: lines
MOLECULE TYPE: cI
IMMEDIATE SOURCE:
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                                      Gaps
                                      0
1.1%; Score 18; DB 4; Length 2311;
100.0%; Pred. No. 36;
tive 0; Mismatches 0; Indels
                                                                                                  908 CGCTATAAAAAGGCGGC 891
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APPLICANT: Charles Kunsch

APPLICANT: Charles Kunsch

Gil H. Choi

Batrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 2; Length 3845;
Pred. No. 35;
0; Mismatches 0; Indels
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                                                                                                    COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC COMPUTER:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,240A
FILING DATE: 29-MAR-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/817,800
FILING DATE: 09-JAN-1992
RIGH APPLICATION DATA:
APPLICATION NUMBER: US 08/167,453
FILING DATE: 15-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 38,153
REFERENCE/COCKET NUMBER: 39151/31958
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                              RY: Unites States of America
60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 520, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1154 CACATAGGCCTTCCTGGC 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMONICATION INFORMATION
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
INFORMATION FOR SEQ ID NO. 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3845 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Watches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
37..3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-956-171E-520
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-220-240A-4
                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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0
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LANG, Florian
APPLICANT: MALDEGER, Tubingen
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 2370; 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marikainen, Marja-Terttu
APPLICANT: Partanen, Juha
APPLICANT: Makela, Tomi
APPLICANT: Makela, Tomi
APPLICANT: Korhonen, Jaana
TITLE OF INVENTION: ANTIBODIES RECOGNIZING TIE RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,295
FILING DATE: 26-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.1%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 36; Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Alitalo, Kari
APPLICANT: Matikainen, Marja-Terttu
APPLICANT: Partanen, Juha
                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08220240A Patent No. 5955291 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFRENCE/DOCKET NUMBER: 05831,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5309
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1501 CGGCTATAAAAAGGCGGC 1518
                                                                                          Sequence 1, Application US/09031295
Patent No. 6326181
                                                                                                                                                                                                                                                                           ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        941 cecratababaececc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2370 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 43..1335
US-09-031-295-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-220-240A-4/c
                                                                       US-09-031-295-1/c
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Gaps

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Gaps
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1.1%; Score 18; DB 4; Length 3982;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6566662el Nucleic Acids and
TITLE OF INVENTION: No. 6566662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARR: Dt. FL. genes Version 1.0
SEQ ID NO 362
LENGTH: 4061
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: RASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-OCt-1997
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                        PRIOR APPLICATION: CURKNOWNS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 06/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARE: J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPHONE: (240) 314-1224
TELEPHONE: (301) 309-8439
INFORMATION FOR SEQ ID NO: 520:
SEQUENCE CHARACTERISTICS:
LENGTH: 3982 base pairs
TYPE: nucleic acid
STADEL CACHARACTERISTICS:
TYPE: nucleic acid
STADEL CACHARACTERISTICS:
TYPE: nucleic acid
STADEL CACHARACTERISTICS:
TYPE: nucleic acid
STADEL CACHARACTERISTICS:
TYPE: nucleic acid
STADEL CACHARACTERISTICS:
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 520:
US-08-956-171E-520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 363, Application US/09620312D; Patent No. 656962; GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Rei, Feiyan
APPLICANT: Ren, Rei, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Rang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
APPLICANT: Zang, Yonghong
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Wang, Zhiwei
John Tillinghast
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; ORGANISM: Homo sapiens
; FEATURE:
; RATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(3062)
US-09-620-312D-363

US-09-620-312D-363

Query Match
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 TAAATTTTATAGTTAGAT 55

Db 3544 TAAATTTTATAGTTAGAT 3561

Search completed: September 2, 2004, 21:26:12
Job time: 152 secs
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Sequence 7252, Ap Sequence 13779, A Sequence 13779, A Sequence 17878, Ap Sequence 5, Appli Sequence 234, App Sequence 151164, Sequence 15164, Sequence 234, Appl Sequence 24699, Sequence 204099, Sequence 204099,
                                                                                                                                    2, 2004, 14:41:35 ; Search time 783 Seconds
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-114-7252

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US-10-732-721-4

US-10-732-721-4

US-10-732-721-5

US-10-198-846-6995

US-10-027-632-151164

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Perfect score:
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15 20 1.2 1979 1.1 1979 1.1 1979 1.2 19	-83	US-10-117-722-838	US-10-094-749-1102	0 - 240 - 453 - 25	9-764-891-650	.0-091-414-27	0 - 293 - 864 - 1	US-10-450-826-83	US-10-027-632-17		US-10-369-493-29761	US-10-027-632-324809	10-027-632-3	10-027-632-	-10-027-632-	10-027-632-7107	10-027-632-7107	10-001-885-1	-10-027-632-	-10-027-632-28824	-10-027-632-	-10-027-632-	-10-027-632-	10-027-632-	10-027-632-	-10-027-632-	-10-027-632-	-10-027-632-3107	10-027-632-	10-027-632-31072	10-027-632-10327
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## ALIGNMENTS

SULT 1: -10-732-721-1 Sequence 1, Application US/10732721 Publication No. US20040163144A1 GENERAL INFORMATION: -10-732-721-1 APPLICANT: -10-732-721-1 APPLICANT: -10-732-721-1 APPLICANT: -10-10-10-10-10-10-10-10-10-10-10-10-10-	Query Match 100.0%; Score 1658; DB 17; Length 1658; Best Local Similarity 100.0%; Pred. No. 0; Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GAATTCACGGCTCACAATACCAGTCATCTACATGATAAATTTTATAGATTACTT 60 	61 CTTGTAATCATTTCAGAGGATGAAAAAAAACGCAAGAAAGCAAATATTTTAAATGAAT 120 	121 GATGCAATATACAAATTAAATTACACAATTATGTAAGATTACATTGTTTAGTTTCATAGA 180 
RESULT 1 US-10-732-721-1 US-10-732-721-1 SEQUENCE 1, A PUBLICACTION N GENERAL INFOR TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV SOFTWARE: PA	Query Match Best Local Matches 165	\$ qa	Qy e	Oy 12

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ug-10-732

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REPERENCE: 38-21(53131)B

CURRENT APPLICATION: NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 918

TYPE: N...
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Sequence 3295, Application US/10425114

Publication No. US200400348881

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 894
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4.0%; Score 66; DB 13; I
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 66; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.2e-10;
Live 0; Mismatches 0;
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US-10-425-114-13779
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US-10-425-114-3295
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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Best Local Similarity 100.0
Matches 40; Conservative
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ORGANISM: Zea mays
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US-10-437-963-17878/c
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION: NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 17878
LENGTH: 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4. Application US/10732721
; Publication No. US20040163144A1
; Publication No. US20040163144A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; CURRENT APPLICATION NUMBER: US/10/732,721
; CURRENT PILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Maize Embryo-Specific Promoter Compositions and Methods for Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REPERENCE: 38-15 (52226) A
CURRENT APPLICATION NUMBER: US/10/732,721
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
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Pred. No. 5.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_23489C.1
US-10-437-963-17878
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays:
US-10-732-721-4
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1089
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Publication No. US2003009974A1

GENERAL INFORMATION

APPLICANT: ALILIE, James

APPLICANT: ALILIE, James

APPLICANT: Way You you you will you wi
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1.3%; Score 21; DB 13; Length 5956;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                 DB 17; Length 21; 5.3;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                 Query Match 1.3%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 5.3 Matches 21; Conservative 0; Mismatches
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SEQ ID NO 234
LENGTH: 5956
                                                               TYPE: DNA
CRGANISM: Zea mays
US-10-732-721-5
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SEQ ID NO 5
LENGTH: 21
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; Publication No. US20020198371A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2002-04-30
; PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR PELING DATE: 2000-04-20
; PRIOR PELING DATE: 2000-04-20
; PRIOR PELING DATE: 2000-03-24
; PRIOR PELING DATE: 2000-03-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR PELING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-10-24
; PRIOR FILING DATE: 1999-108-08
; PRIOR FILING DATE: 1999-108-08
; PRIOR FILING DATE: 1999-108-08
; PRIOR FILING DATE: 1999-09-08-08
; PRIOR FILING DATE: 1999-09-08-08
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                                                                                                                                                                                                                                     LOCATION: 5, 6, 7, 10, 11, 12, 13, 16, 17, 18, 21, 22, 23, 28, 29, LOCATION: 30, 31, 33, 34, 35, 39, 41, 47, 49, 50, 53, 54, 56, 58, LOCATION: 59, 60, 61, 62, 63, 65, 66, 67, 69, 73, 74, 75, 79, 80, LOCATION: 82, 83, 84, 85, 86, 87, 88, 89, 92, 93, 94, 97, 99, 103, LOCATION: 107
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100.0%; Pred. No. 24;
tive 0; Mismatches 0;
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921,
997,
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151164
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6995
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
| NAME/KEY: misc feature
| LOCATION: 109, 110, 111, 112, 113, 114, 120CATION: 204, 228, 406, 811, 870, 914, 120CATION: 972, 977, 980, 983, 994, 995, 10CATION: 1053, 1081, 1083, 1085, 1088 US-10-198-846-6995
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                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                    misc_feature
5, 6, 7, 10,
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Best Local Similarity
Matches 20; Conservat
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US-10-027-632-151164
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US-10-027-632-151164
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Sequence 204099, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: POLY 0.24-30
CURRENT PELLORATION NUMBER: US/10/027,632
CURRENT PELLOR DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR PELLOR DATE: 2000-07-12
FRIOR PELLOR DATE: 2000-04-30
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-8
FRIOR FILING DATE: 1999-09-8
FRIOR FILING DATE: 1999-09-8
FRIOR FILING DATE: 1999-09-8
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FRIOR FILING DATE: 1999-09-8
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FRIOR FILING DATE: 1999-09-9
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FRIOR FILING DATE: 1999-09-9
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Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 1099-11-23
PRIOR PLING DATE: 1099-11-23
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1.2%; Score 20; DB 13;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0
                                  1227 TGAGTTCAACATCTTTCTTA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1770 TTTCCTTAAGAAAAAACA 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1). T. (1924)
OTHER INFORMATION: n = A,T,C or G
900 TGAGTICAACATCTTTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (1)...(1924)
                                                                                                                                                                RESULT 13
US-10-027-632-204099/c
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US-10-027-632-204099/c
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ORGANISM: Human
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| Sequence 13. Application US/10268822
| Publication No. US20030150004A1
| Septence 13. Application No. US20030150004A1
| SEPENCATION:
| APPLICANT: More, David
| APPLICANT: Wei, Ping
| APPLICANT: Chua, Streven
| TITLE OF INVENTION: Screening Systems and Methods for Identifying Modulators of Xenoh
| TITLE OF INVENTION: Metabolism
| FILE REFERENCE: PO2729US2
| CURRENT APPLICATION NUMBER: US/10/268,822
| CURRENT FILING DATE: 2002-010-10
| PRIOR PILING DATE: 2001-09-22
| PRIOR FILING DATE: 2001-09-12
| PRIOR FILING DATE: 2001-09-15
| PRIOR FILING DATE: 2001-09-15
| SEQ ID NO. 13
| LENGTARE: PatentIn version 3.1
| SEQ ID NO. 13
| LENGTH: 1590
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                                                                                                                                                                                                          APPLICANT: Wang, David G.

ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,006
PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-07-12
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PRIOR PLILING DATE: 2000-03-29
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PRIOR PLILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FRAEERE FRAEERE PARKENDE
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100.0%; Pred. No. 24;
tive 0; Mismatches 0; Indels (
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1.2%; Score 20; DB 15; Length 1690;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                      Sequence 151164, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 100.(
Matches 20; Conservative
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; ORGANISM: Human
US-10-027-632-151164
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Search completed: September 2, 2004, 21:49:23 Job time : 788 secs

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1.2%; Score 20; DB 15; Length 1979;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                     DB 16; Length 1924;
25;
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APPLICANT: Tillinghast, John
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
                                                                                                                                                                                                                                                                                                                                                                0; Indels
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1.2%; Score 20; DB

Best Local Similarity 100.0%; Pred. No. 25;

Matches 20; Conservative 0; Mismatches
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CURRENT PELLING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR PELLING DATE: 2000-04-25

PRIOR PELLING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: PL. Genes Version 1.0

SOFTWARE: PL. F. L. Genes Version 1.0

LENGTH: 1979
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2044099
LENGTH: 1924
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US-10-037-270-838/C
US-10-037-270-838/C
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
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                                                                                                                                                                                                                                                                                                                                                                                                          231 TITCCTTAAGAAAAAAAA 250
                                                                                                                                                                                                                 | NAME/KEY: misc_feature
| LOCATION: (1)...(1924)
| CTHER INFORMATION: n = A,T,C or G
US-10-027-612-204099
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Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
Tillinghast, John
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Wang, Jian-Rui
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; LOCATION: (175)..(1053)
US-10-037-270-838
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ORGANISM: Homo sapiens
                                                                                                                                                     TYPE: DNA
ORGANISM: Human
FEATURE:
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APPLICANT:
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             5.1.6
Compugen Ltd
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Maximum DB seq length: 2000000000
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70: cyniz 6/ptodata/2/pna/USG013_COMB
70: cyniz 6/ptodata/2/pna/USG013_COMB
70: cyniz 6/ptodata/2/pna/USG013_C
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

est Local Similarity 100.0%; Pred. No. 0; atches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CACGGCTCACAATACCAGCCATCTACATGTGAAATTTTATAGTTP		AATCATTTCAGAGGATGAAAAAAAAATGGCAAGAAAGCAAATATTTAAAT	TTCAGAGGATGAAAAAAATCGCAAGAAAGCAAATTTTTT	CAAATTTAATTACACAATTATGTAAGAT		81 AATCAATTTCTAGAGTCATAATAATGCCTAAATTAAAATTCTATTCTATTTTCCTT	1	10 AMICAMINEMENTALITATION OF THE PROPERTY OF T	41 AAAAAAACAGCCCATTAAGGGCCCCATTAGAATGCGCGCTGCTTCTTTTTTATATA 30	ACAGCCCATTAAGGGACCATTAGAATGCGCGCTGCTCCATTTTTTTT	CTAGGCCACTCCACCTCGCATGCGTGTTTTTATTAC	rrgrigcreachagecachecachecargearaitrir	SCCGCTGCTTTTGCATTAAGGGTCTAGAGATGTACGAGTGCAA	TAAGGGTCTAGAGATGTACGAGI	TIGGAGGAGTAATTTTTTTAATGCACGGAGGCGCTTTGTATTCCT	CAGCAG	GCCGTGCTTCGTGTACGGCAGTGACGAGGCAGCAGCAGCTCTACGTGC	CGTGCTTCGTGTACGGCAGTGACGAGGCAGCAGCAGCTCTACGTG	GTGCCTGCCGTGATGGCAAGGCTTGCTTGCTTGCGTGCCT	THE CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROL	SAGGITGAAGCIACGCGGTGGCTGCTTGCCTGCGCGCGTGCTAGCACGC	CGAGGTTGAAGCTACGGCGGTGGCTGCTTGCCTGCGCGCGTGCTAGCACG	GACGTCGACGCTGATGCTACGTTGCTACTTTTTGTTTTTCTCTGTGCTTG		NAATAAAGGIGIGIATCICAIGIGATIGAATGGAGGGGGGGGGG	richanchearghantaancaacargratacaarrr	81 ATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGGCGATAAATCTGCTAGGG 84	NATCACATGREATCCCCATCGACTTCGTGTCGGCGATAAATCTG	841 ATTIGIGCITITICAIGIAIGIGCIIGAAIAGAGAGGAAGAATAAATAITACATAAAATAI 900	CATGIATGICTIGAATAGAGAAGAAGAATAATTI	DAACAICTITCITAAIACCTITIGCICGAICTC	rtaaracettttgeregarereerragragaeeer	61 TAACGIGITAAGAACCCTIGITACGAGIGIAGICCAAGGCIGCTIAACIGAATAAIAG 102	61 TAACGTGTTAAGAACCCCTTGTTACCGAGTGTAGTCCAAGGCTGCTTAACTGAATAATAG 102	1021 TAGAACACAAGGAGACAAGAGTGTAGAGAGGAGCTGATTCTTTGTTACTATATGGTGCTG 1080
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Decription	ה ה ה ה ה ה ה ה ה ה ה ה ה ה ה ה ה ה ה	Sequence	Sequence 7324, Ap Sequence 40406, A	Sequence 40406, A Sequence 40406, A	Sequence 30469, A Sequence 74766, A	Sequence 27134, A Sequence 71431, A	Sequence 37309, A	Sequence 7252, Ap	Sequence 9/3, App Sequence 273716,	Sequence 273716, Sequence 13779, A	Sequence 13779, A	Sequence 39577, A	Sequence 39377, A	Sequence 92393, A	Sequence 5/02/, A Sequence 57027, A	Sequence 3994, Ap Sequence 3994, Ap	Sequence 57027, A Sequence 79013, A	Sequence 79013, A Sequence 1774. Ap	Sequence 79013, A Sequence 43255, A	equence equence	Sequence 76235, A Sequence 78600, A	Sequence 78600, A Sequence 3420, Ap	equence equence		ednence					Compositions and Methods for Use						Length 1658;
2		00 US-60-434-242-1 10 US-60-531-039-16	6 US-09-620-111B-7324 8 US-09-304-517A-40406	9 US-09-371-146A-40406 2 US-09-985-678-40406	5 US-09-865-439A-30469 6 US-60-207-458-74766	5 US-09-865-439A-27134 6 HS-60-207-458-71431	6 US-10-155-881-37309	1 US-10-425-114-7252	18 US-60-312-544-973 17 US-09-654-617-273716	:9 US-09-684-016-273716 :1 US-10-425-114-13779	II US-10-425-114A-13779	9 US-09-371-146A-39577	15 US-09-865-676-39577 15 US-09-865-439A-48132	(6 US-60-20/-458-92395 (8 US-09-303-031A-3994	8 US-09-304-517A-57027 9 US-09-371-146A-57027	16 US-09-894-949-3994 16 US-09-894-949A-3994	12 US-09-985-678-57027 8 US-09-304-517A-79013	9 US-09-371-146A-79013	12 US-09-985-678-79013 15 IIS-09-865-439A-43255	0-SU	16 US-60-207-458-76235 -8 US-09-304-517A-78600	US-09-371-146A-7860 US-09-565-306-3420	US-09-985-678-786 US-09-865-439A-44	-207-458-88800 -304-517A-3926	US-09-371-146A-3926	ALIGNMENTS		1434242	1 H H	cific Promoter		R: US/60/434,242 2-12-18	3.2			0%; Score 1658; DB 100;
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				961 TAACGIGITAAGAACCCCTIGITACCGAGGIGIAGGCCCAGGCTTAACIGAAIAATAG 1020	1081 CTCTCCAAAGGTTACATGATATGGGGATCTCCTCTATTTATAGACAAAACTAGGGTTT 1140
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	a & a & a & &	4 6 6 6 6	8 & 8 & 8	90 G	\$6 & \$6
1021 TAGAACACAAGGACAAGAGGAACTGATTCTTTGTTACTATATGGTGCTG	1981 GTUGGGGCTGGGGGGGGGGGCTTGCAATTGGTCGTCGGGTCGGTGGACGTCCCT 14  1441 GGTCGGGTTGCCGGCTTTGCCCTGGCGCGCGACGTGCGGTCGCGTCCCCACGTCCCT  1441 GGTCCGGCTTTGCCGTTGCCCTGGCCTCGCGCGACGTGCCGCGTTCCCCCACGGA 15  1501 GGCTATAAAAAGGCGGCCACCTGATCCTCCATCTCACACAAGCAAG	D 1561 AGCCAACACCTAAAGAACAGTAGTAGTAGTCCCTGTGTACGTAGCAACGATC Y 1621 CCGAGCTCGCCAGTTTTGCTCGTTAGTTTGGACGGC 1658	; APPLICANT: Savidge, Beth; ; APPLICANT: Savage, Thomas ; APPLICANT: Cavage, Thomas ; APPLICANT: Chaudhuri, Sumita ; TITLE OF INVENTION: Materials and Methods for the Modulation of D-type Cyclins in; ; TITLE OF INVENTION: Plants ; FILE REFERENCE: REP. 01-039 ; CURRENT APPLICATION NUMBER: US/60/531,039 ; CURRENT FILING DATE: 2003-12-19 ; NUMBER: OF SEQ ID NOS: 40 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 16	LENGTH: 1658     TYPE: DNA     ORGANISM: Zea mays     S-60-531-039-16     Query Match     Best Local Similarity 100.0%; Score 1658; DB 110; Length 1658;	Valive U; GCTCACAATACCA GCTCACAATACCA GCTCACAATACCAATTCAGAGGATG

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100.0%; Pred. No. 4e-23;
ive 0; Mismatches 0; Indels
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4e-23;
hes 0; Indels
       Sequence 440406, Application US/09304517A;
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: 38-21(15097)B
FILE REPERENCE: 38-21(15097)B
CUTRENT APPLICATION NUMBER: US/09/304,517A
CUTRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 40406
LENGTH: 308
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100.0%; Pred. No. 4e-
:ive 0; Mismatches
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TITLE OF INVENTION: ANNOTATED PLANT GENES
FILE REPERENCE: 38-21(15.097)C
CURRENT APPLICATION NUMBER: US/09/371,146A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR APPLICATION NUMBER: US 09/304,517
NUMBER OF SEQ ID NOS: 294310
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APPLICANT: Cheikh, Uingdong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517.255/38-21(15097)F
CURRENT APPLICATION NUMBER: US/09/985,678
CURRENT FILING DATE: 2001-11-05
PRIOR PPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 40406, Application US/09371146A; GENERAL INFORMATION: ; APPLICANT: Cheikh, Nordine
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Best Local Similarity 100.
Matches 68; Conservative
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Best Local Similarity
Matches 68; Conserv
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CRGANISM: Zea mays
US-09-371-146A-40406
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US-09-371-146A-40406
US-09-304-517A-40406
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US-09-985-678-40406
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LENGTH: 308
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1070P
FULE REFERENCE: 2750-1070P
CURRENT PELLOR DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
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1141 CAGGCATATGGGCCACATAGGCCTTCCTGGCCCAAGAAAGGTTTCTTAACACTACCATCT 1200
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LOCATION: 1..385
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc_feature
LOCATION: 1..385
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8.6e-29;
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V 100.0%; Pred. No. c..
O; Mismatches
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OTHER INFORMATION: Ceres Seq. ID 1339942
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Best Local Similarity
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US-09-620-111B-7324
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LENGTH: 385
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APPLICANT: Aggerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FIRE REPRESENCE: 38-2.1(51936)
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT PILING DATE: 2001-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3354-008-P1-KI-B11
                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.0%; Score 67; DB 76; I
1 Similarity 100.0%; Pred. No. 1.3e-22;
67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 TYPE: DNA
CAGANISM: Zea mays
COTHER INFORMATION: Clone ID: LIB3354-052-P1-K1-G5
US-60-207-458-74766
                     CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
SEQ ID NO 74766
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-865-439A-27134
; Sequence 27134, Application US/09865439A
; GENERAL INFORMATION:
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Conner, Timothy W.
Deikman, Jill
Hardeman, Kristine J.
La Rosa, Thomas J.
          PLANTS
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Best Local Similarity
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              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30469, Application US/09865439A

Sequence 30469, Application US/09865439A

GENERAL INFORMATION:
GENERAL INFORMATION:
Michael D

APPLICANT: Hardeman, Kristine J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, La Rosa, Thomas J.

APPLICANT: La Rosa, La 
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4.1%; Score 68; DB 42; Length 308;
Best Local Similarity 100.0%; Pred. No. 4e-23;
Matches 68; Conservative 0; Mismatches 0; Indels
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4.0%; Score 67; DB 35; I
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 67; Conservative 0; Mismatches 0;
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US-09-865-439A-30469
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ruan, Yijun G.
APPLICANT: Ruan, Yijun G.
APPLICANT: Sammons, R. Douglas
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Wu, Kunsheng
APPLICANT: Xu, Nanfei
TITLE OF INVENTION:
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NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 40406
LENGTH: 308
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US-09-985-678-40406
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ORGANISM: Zea mays
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US-60-207-458-74766
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APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DAFE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 7252

TYPF: No. 7252
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APPLICANT: Elou, Yibua
APPLICANT: Elou, Yibua
APPLICANT: Sorven, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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4.0%; Score 67; DB 51; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 836;
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4.0%; Score 67; DB 51; Length 83
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 67; Conservative 0; Mismatches 0; Indels
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US-10-425-114-7252
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US-10-425-114A-7252
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US-60-312-544-973
; Sequence 973, Application US/60312544
; GENERAL INFORMATION:
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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LENGTH: 836
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GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton B.
APPLICANT: Liu, Jingdong
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: NUMBER: US/10/155, 881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NOS: 37595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 67; Conservative 0; Mismatches 0;
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OTHER INFORMATION: Clone ID: LIB3354-008-P1-K1-B11
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Wu, Kunsheng
APPLICANT: Wu, Nanfei
APPLICANT: Xu, Nanfei
TITLE OF INVENTION: PLANTS
FILE REPERENCE: 38-21(51936)A
CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
                                                                                                                                                                                         Lalgudi, Raghunath V.
Ruaf, Yijun G.
Rutf, Thomas G.
Sammons, R. Douglas
Shukla, Hridayabhiranjan
Wu, Kunsheng
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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; ORGANISM: Zea mays
US-10-155-881-37309
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US-10-425-114-7252
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1553 GCAGCAACACCCAACACCTAAACTAAAGAACAGTAGTAGTCCCTGTGTACGTCTAGCAAC 1612
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Honkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INTENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(5272,544
CURRENT APPLICANTON NUMBER: US/60/312,544
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 973
LENGTH: 836
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APPLICANT:
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APPLICANT:
APPLICANT:
TITLE OF INVENTION:
Annotated Plant Genes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS:
LENGTH: 861
                                                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
; LOCATION: (108)...(449)
; CTHER INFORMATION: Clone ID: 700623908_FLI
US-60-312-544-973
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                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Zea mays FEATURE:
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CRGANISM: Zea mays
US-09-654-617-273716
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1554 CAGCAACAGCCAACACTAAACTAAAGAACAGTAGTAGTCCCTGTGTACGTCTAGCAACG 1613

Query Match 4.0%; Score 66; DB 27; Length 861; Best Local Similarity 100.0%; Pred. No. 4.4e-22; Matches 66; Conservative 0; Mismatches 0; Indels

0; Gaps

24 CAGCAACAGCCAACACTAAACTAAAGAACAGTAGTAGTCCCTGTGTACGTCTAGCAACG 83

1614 ATCCGC 1619

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84 ATCCGC 89

Search completed: September 2, 2004, 21:23:30 Job time: 4955 secs

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- nucleic search, using sw model OM nucleic

September Run on:

2, 2004, 13:36:00 ; Search time 586 Seconds (without alignments) 9801.724 Million cell updates/sec

US-10-732-721-1 1658 Title: Perfect score:

1 gaattcacggctcacaatac......tctcgttagtttgggacggcg 1658 OFIGO NAC Scoring table: Sequence:

residues 5837357 seqs, 1732150321 Searched:

Gapop\_60.0 , Gapext 60.0

0 Word size : Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*

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5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
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8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq2:\*
9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		UB ID Description	7 US-10-732-721-1 Sequence 1. Appli	US-10-425-115-181022 Segmente 18	US-10-425-115-181033 Sequence	US-10-425-115-47987 Seguence	US-10-425-115-82158 Sequence	US-10-425-115-68623 Sequence	US-10-732-721-4 Segmence 4.	US-10-732-721-5 Sequence 5	US-10-425-115-30821 Sequence 30	US-10-918-754-16910 Segmence	US-10-918-754-16866 Segmence	US-09-865-590A-3153 Seguence 3153. A	US-10-425-115-12790 Sequence	US-10-425-115-163648 Sequence	Sequence	PCT-US04-07412-1190 Sequence 119	US-10-389-559-1190 Seguence 1190,	US-10-472-965-729 Sequence 729, 1	US-10-896-164-8392 Seguence 8392	US-10-896-164-11776 Sequence	US-10-868-184A-8392 Sequence 8392	US-10-868-184A-11776 Sequence	US-10-868-184-8392 Segmence	
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-915-727-12219	US-60-568-845-11203	US-60-568-845-11242	US-10-674-124A-17773	US-10-425-115-120930	US-09-949-003C-25389	US-09-949-003C-25390	US-09-949-003C-25391	US-09-949-003C-28894	US-09-949-003C-28895	US-09-949-003C-28896	US-10-767-701-8179	US-10-425-115-146524	US-60-579-062-25357	US-10-425-115-94611	PCT-US04-05654-2721	US-10-896-164-8129	US-10-868-184A-8129	US-10-868-184-8129	US-60-563-440-12172	US-60-563-440-12170
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20	13	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19
25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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RESULT 1

US-10-732-721-1

US-10-732-721-1

Sequence 1, Application US/10732721

SEQUENCE 1, Application US/10732721

SEQUENCE 1, Application US/10732721

SEQUENCE 1, Application Sequence 1

TITLE OF INVENTION: Maize Embryo-Specific Promoter Compositions and Methods for Use 1TITLE OF INVENTION: Thereof 1

FILE REFERENCE: 38-15 (52826) A

CURRENT APPLICATION WUMBER: US/10/732,721

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-18

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Similarity
Matches 1658; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Zea mays US-10-732-721-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cov. Yihua
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SUC ID NOS: 369326
SEC ID NO 47987
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| Sequence 82158, Application US/10425115
| Sequence 82158, Application US/10425115
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: US/10/425,115
| CURRENT APPLICANT: AP
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               2.4%; Score 40; DB 6; Length 1034; 100.0%; Pred. No. 5.9e-10; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.4e-09;
tive 0; Mismatches 0;
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2.2%; Score 37; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 37; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_14376C.1 US-10-425-115-47987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(528)
OTHER INFORMATION: unsure at all n locations
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Query Match
Best Local Similarity 100.0
Matches 40; Conservative
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Best Local Similarity 100.0
Matches 38; Conservative
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ORGANISM: Zea mays
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US-10-425-115-47987/c
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ORGANISM: Zea mays
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RESULT 7
US-10-732-721-4
US-10-732-721-4
Sequence 4, Application US/10732721
Sequence 4, Application US/10732721
GENERAL INFORMATION:
TYLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
FILE REFERENCE: 38-15 (52826) A
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
ILENGTH: 21
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TITLE OF INVENTION: Maize Embryo-Specific Promoter Compositions and Methods for Use
TITLE OF INVENTION: Thereof
FILE REPERBNCE: 38-15 (52856)A
CURRENT APPLICATION NUMBER: US/10/732,721
                                                                                               Sequence 68623, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cav. Youlas
APPLICANT: Cav., Youlawit
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222)
FURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 68623
LENGTH: 868
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100.0%; Pred. No. 0.46;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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2209 AAGGTTACATGATATGGGGATCTCCTCTCTATTTATA 2173
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100.0%; Pred. No. 4.3;
ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_162578C.1 US-10-425-115-68623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 AGTCATCTACATGTGATAAATTT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 AGTCATCTACATGTGATAAATTT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1226 ACTCCTTCCCTCCGCCTCCAG 1246
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                           RESULT 6
US-10-425-115-68623/c
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ORGANISM: Zea mays
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RESULT 12
US-09-865-590A-3153
US-09-865-590A-3153
SEGRETAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard
TITLE OF INVENTION: Novel Human Polynucleotides and Polypeptides Encoded Thereby
TILE REFERENCE: 21402-016
CURRENT APPLICATION NUMBER: US/09/865,590A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/206,132
PRIOR APPLICATION NUMBER: 60/228,716
PRIOR APPLICATION NUMBER: 60/228,716
PRIOR APPLICATION NUMBER: 60/228,716
PRIOR APPLICATION NUMBER: 60/228,716
SEQ ID NOS: 22982
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3153
LENGTH: 291
                                                                                                                                                                                                                                    RESULT 11
US-10-918-754-16866/c
Squence 16866, Application US/10918754
; SGQUENCE 16866, Application US/10918754
; GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DEST THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REPREBRICE: CLO01480
; CURRENT PAPLICATION NUMBER: US/10/918,754
; CURRENT PILING DATE: 2004-08-16
NUMBER OF SEQ ID NOS: 91238
; SCFTWARF FALLING DATE: PARESEQ for Windows Version 4.0
; SEQ ID NO 16866
LENGTH: 244289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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100.0%; Pred. No. 6.6;
.ive 0; Mismatches 0; Indels 0
Query Match
1.3%; Score 21; DB 6; Length 88344;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 16;
tive 0; Mismatches 0; Indels
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; LOCATION: (274)..(274)
; OTHER INFORMATION: Wherein n may be a, c, g
US-09-865-590A-3153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47515 AAGAAAGCAAATATTTTAAAT 47495
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                                                                                                            96 AAGAAAGCAAATATTTAAAT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 TCATTTCAGAGGATGAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3 Best Local Similarity 100. Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-918-754-16910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-425-115-30821
; Sequence 30821.
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Low (xoalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Plants
; TILLE OF INVENTION: Plants
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: 38-21(5322)B
; CURRENT FILLING DATE: 2003-04-28
; SEQ ID NO 30821
. LENGTH: 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-918-754-16910/c

| Sequence 16910, Application US/10918754
| Sequence 16910, Application US/10918754
| Sequence 16910, Application US/10918754
| Sequence 16910, Application US/10918754
| Sequence 16910, Application US-10018 | Sequence 16910, Application US-10018 | Sequence 16910, Application US-10018 | Sequence INVENTION: USES THEREOF
| FILLE OF INVENTION: USES THEREOF
| FILLE REPERRACE: CLO01480
| CURRENT APPLICATION NUMBER: US/10/918,754
| CURRENT PILING DATE: 2004-08-16
| NUMBER OF SEQ ID NOS: 91238
| SOFTWARE: FastSEQ for Windows Version 4.0
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1.3%; Score 21; DB 6;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_128119C.1 US-10-425-115-30821
                                                                                                                                                                                                                                                                         Query Match 1.3%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 4.3 Matches 21; Conservative 0; Mismatches
                  PRIOR APPLICATION NUMBER: US/60/434,242
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SCFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 21
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                                                                                                                                                                            ; TYPE: DNA; CRGANISM: Zea mays
US-10-732-721-5
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Gaps

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1.2%; Score 20; DB 1; Length 1690;
100.0%; Pred. No. 18;
tive 0; Mismatches 0; Indels
         PRIOR APPLICATION NUMBER: PCT/US 01/29672
PRIOR FILING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR FILING DATE: 2001-010
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-08-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SOFTWARE: PATENTIN VERSION 3.1
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Job time: 588 secs
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Mouse
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APPLICANT: Wei, Ping
APPLICANT: Wei, Ping
TITLE OF INVENTION: Screening Systems and Methods for Identifying Modulators of Xenob
TITLE OF INVENTION: Metabolism
FILE REPERENCE: P027-29002
CURRENT APPLICATION NUMBER: PCT/US03/32273
CURRENT FILING DATE: 2003-10-09
              Sequence 12796, Application US/10425115
GRNERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Younged:
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 18-21 (33.22) BCURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 12790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La ROSa, Thomas J.
APPLICANT: La ROSa, Thomas J.
APPLICANT: La ROSa, Thomas J.
APPLICANT: Shou, Yihwai
APPLICANT: Zhou, Yihwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 [53222] B
CURRENT FILING DATE: 2003-04-28
SUMBER OF SEQ ID NOS: 369326
SEQ ID NO 163648
LENGTH: 955
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100.0%; Pred. No. 17;
cive 0; Mismatches
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Pred. No. 17;
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US-10-425-115-12790
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V 100.0%; Pred. No. 1.,
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US-10-425-115-163648
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US-10-425-115-163648
; Sequence 163648, Application US/10425115
; GENERAL INFORMATION:
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FT-US03-32273-13/c
; Sequence 13, Application PC/TUS0332273
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 rGATAACGTGTTAAGAACCC 742
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Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Zea mays
FEATURE:
US-10-425-115-12790
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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PUJCV14TD OGUDK20TV PUCEI43TD

PUIIU51TB PUFPD96TD

PUFPD96TB PUJDJ37TB PUJDJ37TD PUHDX59TD

PUFUD53TB PUJFD11TB PUFUD53TD

PUDIN46TD

PUFVU43TB PUFWI17TD hn38d06.b PUBND60TD

Zea mays

PUBNEGOTD

PUFYZ51TB PUFYZ51TD PUFVU43TD 687029C03 PUECF15TD 614097C04 PUDIU72TD

PUJGY13TD PUEIE27TD PUGAG16TB

ZMMBBc034 PUFED34TD PUFWE84TB PUFUA36TB

PUFWI17TB

OGUMP60TV OG1AE48TV

OG1AE48TH

ZMMBBb013

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CC418961 179 bp DNA linear GSS 19-MAY-2003 PUEDX81TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa230M18,
                                                                                                                                                                                                                                                                                                                                                                  Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 779)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reshick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
CG146205
CC654144
BZ70562075
CG164746
CG062075
CG193723
CG193723
CG096594
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Fax: 301-838-0208
Eaxi: 301-848-0208
Eaxi: 301-18-whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                           ALIGNMENTS
     CC654144
BZ705097
CG164746
                         CG062076
CG062075
CG193723
CG193725
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CG096596
AY106704
CG118361
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CG175932
CG175933
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BZ828297
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CG097258
CG050059
CG050060
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BZ961663
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                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
CC418961
CC418961.1 GI:30899051
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Contact: Cathy Whitelaw
GSS.
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                              RESULT 1
CC418961/c
LOCUS
DEFINITION
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JOURNAL
COMMENT
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AUTHORS
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                                         2, 2004, 10:46:24 ; Search time 3928 Seconds (without alignments) 12604.760 Million cell updates/sec
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                            nucleic search, using sw model
                                                                                                                   27513289 segs, 14931090276
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gb_est2:*
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gb_est4:*
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728
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754
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26.3
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                                                                    Title:
Perfect score:
                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451
436
374
313
                             OM nucleic
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Database :

Result No.

1264

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Word size

Searched:

Sequence:

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Run

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CG151999 498 bp DNA linear GSS 21-AUG-2003
PUIFT17TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0573C10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1140 TCAGGCATATGGGCCACATAGGCCTTCCTGGCCCAAGAAAGGTTTCTTAACACTACCATC 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 TAACGTGTTAAGAACCCCTTGCTACCGAGTGTAGTCCAAGGGCTGCTTAACTGAATAATA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICCAGGCGCGCGTCGTGCTTCAACTCCTTCCCTCCGCCTCCAGAGCGGATAAATA 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901 GAGTICAACAICTITCTIAATACCTITIGCTCGATCTCCTTAGTAGAGCCACGTGCGTGA 960
                                                                                                                                                                                                                                                        /db_xref="taxon:4577"
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/clone=lih="zm_0.6_1.0_KB"
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CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 ATCAGTAACACATCACCATCCCCATCGACTTCGTGTCGGCGATAAATCTGCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 ATTIGIGCTTTTCAFGTATGTGCTTGAATAGAGAGAAAGAATAATACATAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 GIAGAACACAAGGACAAGAGTGIAGAGAAGGAACIGAITCITIGITACTAATATGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 GCTCTCCAAAGGTTACATGATATGGGGATCTTCTCTCTTTTTTATAGACAAAACTAGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGGCATATGGGCCACATAGGCCTTCCTGGCCCAAGAAAGGTTTCTTAACACTACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 GACGTCGACGCTGATGCTAGCGTACCTTTTGTTTTTGTTTTCTCTTGTGCTTGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCAGTAAAATAAACGTGTGTATCTCATGTGATTGATCGACGTGTGTCGCGCGATTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 ATCAGTAACAATCACATGTGCATCCCCATCGACTTCGTGTCGCGATAAATCTGCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841 ATTIGIGCTITICATGIATGIGCTIGAATAGAGGAAAGAATAATATTACATAAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 GAGTICAACATCITICITAATACCITITIGCICGATCICCITIAGIAGAGCCACGIGCGIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAACGTGTTAAGAACCCCTTGTTACCGAGTGTAGTCCAA-GGCTGCTTAACTGAATAATA
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 728,
                                   9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Fax: 301-838-0208
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.3%; Score 436; DB 29;
Best Local Similarity 99.5%; Pred. No. 6.4e-196;
Matches 656; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                       DNA"
                                                                                                                                                                                              /organism="Zea mays"
/mol_type="genomic Di
/strain="B73"
                                                                                                                                                           Location/Qualifiers
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
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CG151999
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DEFINITION
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                502 GCATGCGTGTTCTTTATTACATGAAAAATGAGCCGCTGCTTTTGCATTAAGGCCCTAGA 443
                                                                                                                                                                                                                                                                                                                                                                                                                            323
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                                                                                                   /db_xref="taxon:4577"
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CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGCAGCTCTACGTGCCCACGTGCCTGCCTGCCCACCGTGATGGCAAGGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCGCGCGTGCTAGCACGCCGACGACGTCGACGCTGATGCTAGCGTTGCTACTTTTGTTT
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                         Length 779;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                            Score 451; DB 28;
Pred. No. 4.6e-203;
                                                                                                                                                                                                                                         27.2%; Score 451; DB
llarity 99.8%; Pred. No. 4.6e
Conservative 0; Mismatches
                                                         /mol_type="genomic DNA"
/strain="B73"
                                           'organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCGGCGATAAATCTGCTAGG 839
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUIFT17TB
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CG152000
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                                                                                                                                                                                                                                                                  Local
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KEYWORDS
SOURCE
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CG152000/c
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JOURNAL
COMMENT
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        FEATURES
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754 bp DNA linear GSS 21-AUG-2003 PUCCY14TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0639C04, Genomic survey sequence. CG146202 CG146202.1 GI:34036985 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 754)
Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T., Benick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUCVU4TD /mol\_type="genomic\_DNA"

/kstain="B73"

/db\_xref="taxon:4577"

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/clone="Lb="ZM\_0.6\_1.0 KB"

/note="Vector:"PCR4-TOPO, Site\_1: EcoRI; 0.6-1.0 kb high

COT selected genomic\_DNA library" 9712 Medical Center Drive, Rockville, MD 20850, USA 1. .754 /organism="Zea mays" Class: sheared ends. Location/Qualifiers Email: whitelaw@tigr.org Tel: 301-838-5843 Fax: 301-838-0208 Seg primer: TR Zea mays Zea mays TIGR GSS. LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE CG146202/c ORGANISM TITLE JOURNAL REFERENCE AUTHORS FEATURES COMMENT RESULT ORIGIN

Gaps .. 0 Length 754; 1; Indels 18.9%; Score 313; DB 29; ilarity 99.7%; Pred. No. 1.9e-137; Conservative 0; Mismatches 1; Similarity 363; Query Match Best Loca Matches

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1311 1312 GGGAATGCGCGCAGGCCATCGCTCGACACGCACGTACGTGTCGCCCCCGCGAGGCCTCCT 1371 CGCACACGCGTCGCGCCGCACGGGCGCCCGAGGGACCTTGCAATTCGTCCGCGTCGGTGCA 1431 1492 CCCACCGGACGGCTATAAAAAGGCGGCCACCTGATCCTCCATCTCACACAAGCAAAGC 1551 245 364 ATAAATACGGGGTCTACGGTGCACGCGCACGCACGCGCCGAGGGCATCTCTGCCCG 305 244 CGCACACGCGTCGCGCCCCACGGGCGCCGAGGGACCTTGCAATTCGTCCGCGTCGCTGCA 185 184 cacciccrescrescriscescritecescritescerescrices 65 1252 ATAMATACGGGGTCTACGGTGCACGCACGCATGGTGCGCCGAGGGGCATCTCTGCCCG 304 GGGAATGCGCCCAGGCCATCGCTCGACACGTACGTGTCGCCCCCCGCGAGGCCTCCT 1372 g  $\delta$ g ò d ò g qq à ò g

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TCGAC 498

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PUCEI4JTD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTal27Gl3, BZ705097
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                               1 (Dases 1 to 373)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Vunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGCAATICGICCGCGICGGIGCACACGICCCIGGICCGGCIIGCCGGCTIIGCCCTGGC
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/clone lib="ZM 0.7 l.5 KB"
/note="vector: pBGZK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Best Local Similarity 99.7%; Pred. No. 4.1e-122;
Matches 331; Conservative 0; Mismatches 1;
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/mol_type="genomic DNA"
/strain="B73"
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GSS.
genomic survey sequence.
                                                                                                                                                                                                                                   Unpublished (2002)
Contact: Cathy Whitelaw
                               GI:32057168
                                                                                                                                                                                                                                                                                                                                                      Seq primer: TF
Class: sheared ends.
                               CC654144.1
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            938 bp DNA linear GSS 21-AUG-2003 genomic clone ZMMBTa0639C04, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
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/strain="B73"
/db kraf="taxon:4577"
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/clone="ZMMBTa0639C04"
/note="Wetcr: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
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18.4%; Score 305; DB 29;
Best Local Similarity 99.7%; Pred. No. 1.1e-133;
Matches 355; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                          Other GSSs: PUJCV14TB
Contact: Cathy Whitelaw
                                                                                                        CG146205.1 GI:34036988
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                                                                                                                           GSS.
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786 bp DNA linear GSS 19-AUG-2003 PPRDPSGTD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0701024, GG062076 CG062076 CG062076 GG062076 GG062076
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(bases 1 to 786)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                  /clone="ZMMBTa0593105"
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CoT selected genomic DNA library"
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/note="Vector: pcR4-TOPO; Site 1: BcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone="ZMMBTa0701024"
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Class: sheared ends.
Location/Qualifiers
1. .78
/organism="Zea mays"
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Class: sheared ends.
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Unpublished (2003)
Other_GSSs: PUFPD96TB
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                            Other GSSs: PUIIU51TD
Contact: Cathy Whitelaw
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        Unpublished (2003)
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Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 949)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 CTIGIAATCATITCAGAGGAIGAAAAAAATGCGAAGAAAGCAAATATTITAAATGAAT 290
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Paniciae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4577"
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/clone_lib="xxx=0.6_1.0 xB"
/note="Vector: pCR4_TOF0; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Mitclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J..
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                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="B73"
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Seq primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
                                                                                                                                                                Maize Genomics Consortium Unpublished (2003)
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                                                                                                                                                                                                               Contact: Cathy Whitelaw
TIGR
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                                                                                                                                                     Bennetzen, J.
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es 248; Conserv
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spernatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

( Dases 1 to 438)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4577"
/clone="zmMBTa0642H02"
/clone="tzmMBTa0642H02"
/clone_lib="zm_0.6_1.0_KB"
/note="Tector: pCR4_TOPO; Site_1: EcoRI; 0.6-1.0 kb high
cor_selected_genomic_DNA_library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA Fel: 301-838-9843 Fax: 301-838-0208 Email: whitelaw@tigr.org
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .438
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Unpublished (2003)
Other GSSs: PUJDJ37TD
Contact: Cathy Whitelaw
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CG193725
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Contact: Cathy Whitelaw
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                  GI:34084784
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Class: sheared ends.
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Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                                                                                                                                                                                                        CG062075 858 bp DNA linear GSS 19-AUG-2003 PUFPD96TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0701024,
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                                                                                                                       1037 AAGAGTGTAGAGAGGAACTGATTCTTTGTTACTATATGGTGCTGCTCTCTCCAAAGGTTACA 1096
                                                                                                                                          519 AAGAGTGTAGAGGAACTGATTCTTTGTTACTATATGGTGCTGCTCCCAAAGGTACA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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/db xref="taxon:4577"
/clone="ZMMBTa0701024"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cor selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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                                       Length 786;
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                                       ch 4.0%; Score 67; DB 29; I
1 Similarity 100.0%; Pred. No. 1.8e-20;
67; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Unpublished (2003)
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CG062075
CG062075.1 GI:33934255
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TIGR
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Best Local Similarity 100.0
Matches 67; Conservative
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                                         Query Match
Best Local Similarity
Matches 67; Conserv
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Zea mays
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CG062075
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1130 AACTAGGGTTTCAGGCATATGGGCCACATAGGCCTTCCTGGCCCCAAGAAAGGTTTCTTAA 1189
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                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Viridiplantae; Streptophyta; Esparantophyta; Bagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 884)
1 (bases 1 to 884)
1 hitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
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  321 CTCCAAAGGTTACATGATATGGGGATCTCCTCTCTATTTATAGACAAAACTAGGGTTTCA 262
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    (bases 1 to 844)

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/db xref="than=nB73"
/clone="ZNMBTa219G20"
/clone="ZNMBTa219G20"
/clone="Lb="ZM O.6 1.0 KB"
/note="WetCur: pCR4 TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                         CC006284 BB DNA linear GSS 31-N
PUDIN46TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa219G20,
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Fax: 301-838-0208
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Similarity 100.0%; Pred. No. 4.6e-19;
4; Conservative 0; Mismatches 0;
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                  genomic survey sequence.
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CC006284.1 GI:29384846
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CG096594
CG096594.1 GI:33978888
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1 (bases 1 to 732)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                          /clone="ZMMBTa429122"
/clone_lbb="ZM 0.6 1.0 kB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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PUHDX59TD ZM_0.6_1.0_KB Zea mays genomic clone ZMWBTa429122.
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100.0%; Pred. No. 4.9e-19;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            Length 446;
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                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 5.9e-19;
tive 0; Mismatches 0;
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/mol_type="genomic DNA"
/strain="B73"
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                Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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Class: sheared ends.
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....hes 64; Conservative
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Matches 64; Conserv
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CC352433/c
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FEATURES

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REFERENCE

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Contact: Catny Whitelaw
TIGR
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-2843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 44
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFUD53TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 844;
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